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Ketogulonigenium shuttle vectors

Ketogulonigenium shuttle vectors

Patent: WO 0177347-A I 18-OCT-2001;

Archer-Daniels-Midland Company (US)

Location/Qualifiers

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AE005932 Caulobact
AX083744 Sequence
AX278115 Heliocida
AL669833 Mus muscu
AE004992 Halobacte
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D'Elia,

John

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PAT 02-NOV-2001

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Sequence 3 from Patent W00177347.
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Patent: WO 0177347-A 3 18-OCT-2001;
Archer-Daniels-Midland Company (US);
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1841		ДЬ
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į.	1 ttcccagaagcgggcgggatcacctacagtccacgttggctggagctgaaacgctctgct	Qy
1721	2 GGTTCCAAGGTCGGTCGAGATGCTCGTCGCAGAGGGGCAGCGGAAACGATAGCCCCCTCC	DЬ
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1361		Ъ
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MICHIGAN STATE UNIVERSITY (US); Arche
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Schmidt, T.M. and Stoddard, S.F.
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aaatgacctcagaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
Mammalia; Eutheria; Primates; Catarrhini; Callahan,C., Ho
Indersoll-Ashworth,R.G., Rosenblatt,A., Callahan,C., Ho
Indersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Bri
Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3
associated with Huntington disease-like 2
associated with Huntington disease-like 2
AL Nat. Genet. 29 (4), 377-378 (2001)
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patent: WO 9940220-A 1 12-AUG-1999;
GAUTHIER JEAN MICHEL (FR); GLAXO GR
Location/Qualifiers
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/db_xref="taxon:32630"
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Submitted (05-007-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
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/product="junctophilin 3"
complement(<36507. .>3688
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/db_xref="taxon:9606"
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Disease-Like 2 (HDL2)"
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AX024376
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Patent: DE 19846493-A 13-APR-2000;
BIOTECHNOLOG FORSCHUNG GMBH (DE)
Bacteria; Proteobacteria; Myxococcales; Sorangineae; 1 (bases 1 to 1969)
                                         Polyangium cellulosum Polyangium cellulosum
                                                                                             Sequence 74
AX024269
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/db_xref="taxon:56"
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                       aattgcacagagtgtttcctcccatttcaaagaaatacaccgaaacacctaacacgcaag 1773
                                                                                                                      cggctggacaggctgcaaaagcaacgggtgtggcgaccgcaaccatcactcgggcgctaa 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAACCGCCGAGTCCCACCACGAAGAGCCTGAGCTCCTG
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                                                                      aaagcggtaaaatttccggtaaaaaagatgaatctggggcatgggttatagatcctgcag 1713
                                                                                                                                                   GAGCAGAAACACGATCGGCACCACGAGCGTGAGCTCGAGCAGCGATATTTCATGACCGAC
111;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
I66494
                                                                                                                                                                                                                                                                                                                             Dorner, F., Scheiflinger, F. and Falkner, F. Recombinant fowlpox virus Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOTECHNOLOG FORSCHUNG GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beyer, S. and Mueller, R.J.
Patent: DE 19846493-A 74 13-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beyer,S.
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14 from patent US 56
                                                                                                                                                                                                                                                                             /organism="unknown"
1491 c 1486 g
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/db_xref="taxon:56"
585 c 591 g 376 t
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                                                                                                                                                                                                   2.2%; Score 45.8; D
3.8%; Pred. No. 0.35;
rative 205; Mismatches
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                                                                                                                                                                                                                                                                              368 others
                                                                                                                                                                                                                           Length 7218;
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                                                source
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The true left end of clone C25G4 is at 32680 in this sequence. The true right end of clone F28D1 is at 725 in this sequence. The start of this sequence (1. .103) overlaps with the end of sequence Z70684 The end of this sequence (32680. .32784) overlaps with the start of
                                                                overlapping sections once, or longer becoverlap between neighbouring submissions Location.Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone F08G5. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-APR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 18A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Caenorhabditis elegans
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Caenorhabditis elegans cosmid F08G5,
                                                                                                                                                                                                                                                                                                                                                                                                                                     neighbouring submissions. The true left end of clone F08G5 is at 1 in this sequence. The true right end of clone F08G5 is at 7448 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coding sequences below are predicted from computer analysis, predictions from Genefinder (P. Green, U. Washington), and ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steward, C.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available information.
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                                                                                                                                                                                                                              see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                            For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                 sequence 270680
                                                                                                                                                      the specified clone
                                                                                                                                                                                   IMPORTANT:
                                                                                                                                                                                                           name=F08G5
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/organism="Caenorhabditis elegans'
/db_xref="taxon:6239"
                                                                                                                        This sequence is NOT necessarily the entire insert of ed clone. It may be shorter because we only sequence sections once, or longer because we arrange for a sma
                                                     .32784
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/chromosome="IV" /clone="F08G5"

join(2838. .2935,2985.

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join(2838. .20:
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/gene="r08G5.2"
join(4263. .4329,4376. .4555,4855.
5788. .5943)
/gene="r08G5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted using tRNAscan-SE-1.11
preliminary prediction
similar to tRNA-Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8357. .8473))
Respectively.
Re
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PSDMILIGFHILIMGLFALLVIFLLSFYY"
complement()oin(8848. .6998,7613. .7761,7964. .8053,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="sptrembl:Q19221"
/translation="mearnnwkkqgwpildnviscillvyagivtaficpivelcefy
/translation="mearnnwkkqgwpildnviscillvyagivtaficpivelcefy
TAAPIMLFSTEFRKFVMKIMARAGNLQFITCVRITGIKVMMSGDGLERUTDCRALLLR
RHAGLEDHFIEMTAADSFGVMAVGRWIFVIYMWIYSPLGWLWSSYCMYETIOSVPPHK
RHAGLEDHFIEMTAADSFGVMAVGRWIFVIYMWIYSPLGWLWSSYCMYETIOSVPHK
RAQTLHSLRRHFDRIYHEVDLRWLCLYPEGSRLFLIQKRNSEFEKKRGLPPLTNCAYP
RLGAALSAIKYLGPDDNNPLKSNNGKQPPLETLVDVTLGYPDGNILDLNEIFMSAWRN
                                                                                                                                                                                                                                                            /gene="F08G5.t2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(11009..11080)
/gene="F08G5.t2"
/note="TTG Gln Q-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(10702. .10773)
/gene="F08G5.t3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10702. .10773)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mSYQHEVVKYAPTEDNEIHALIRGKPSFCKANIRVNTQQFQERLTYLDKRYDHLRKMTHSLRKKVNELEDIMRLDNEENMDTIQKLLDEIKREKQLMRDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8357. .8473))
/gene="F08G5.3"
/note="predicted using Genefinder"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(4263. 5788. .594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERFDDPAFLRRYIKRVMSDSKMARLVGMMRSEIRKLPNDEFDAFYKKVKDHQRTAPSS
SKKLGPPAIVQQTSDMEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSQPTSFSQPCDIDIGGSVKKSAARNLSHTYSTNIGESSRMPALTANEFFSQPVYNPY
NRPASSASTVSSSIGSAYSVLHDDSPFSGFSPNSNHSLQFPCPSPSHSSSFSGFSQSS
SHSSQLSSSPANAPSFPDFHSPPSANDIQIDQLNPVTVAPQIKQTADKCVQTDKQYVD
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/translation="meynskktayisetpykdhlnrsstntdvmynsvekrkeges"
// CACAGETPIETRE | The control of the 
                                                                                                                                                                complement(11686. .11758)
/gene="F08G5.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                             similar to tRNA-Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA94582.1"
/db_xref="GI:3875591"
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/protein_id="CAA94584.1"
                                                           predicted using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary prediction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tRNA-Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F08G5.t3"
/note="CTG Gln Q-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIIKGELSKTMYNEDLRRRLAGEWKKIDADRKSSAAESEASSSMIGDDDTPSTSSDGH
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/note="predicted using Genefinder"
                                                                                                           /note="ACG Arg R-tRNA
                                                                                                                                                                                                                                                                                                                                                                       /product="tRNA-Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q19219"
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                                                                tRNAscan-SE-1.11
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Best Local S
Matches 62
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l Similarity
62; Conserv
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/GL_XTOTE SUTTEMBL:Q19222"
/CLTANS AT A CONTROL OF THE CONTROL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Genefinder contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=96.9, E-value=1.3e-25, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=107.1, E-value=1.1e-28, N=1 cDNA EST yk204e8.3 comes from this gene cDNA EST yk204e8.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AICKALNPDAEMASFHSQAESIFVANKYSTIHAWYWIISNSAPSDADSSCVEMMDGLL
GLIFALSLQKGQTNAYSCDESIQIICKYCPRETTSTTTVTPTTTKAATIKTSTTTVTP
TTVTTTKAPTTTKTSTSTTTPKFTTTT]QTTKKITTSPTSTTASIPITCTSNCPVPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SW:UDBE_RABIT), contains similarity to Pfam domain: pF00059 (Lectin C-type domain), Score=15.2, E-value=0.00032, N=1; pF00201 (UDP-glucoronosyl and UDP-glucosyl transferases), Score=104.2, E-value=8.3e-29, N=1
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GAPGAPGDDGHAGEAGKTGINGISLISHEGESGCIKCPAGEAGPAGPDGAPGAPGAPGPDG
QPGQDGPAGQPGAPGPAGPEGDAGAPGAGAPGAPGAPGQDGQRGTGLPGAPGAPGAPGPQ
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/gene="F08G5.4"
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/gene="F08G5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                  30196. .30308,
/gene="F08G5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFKGLCYKMCRGLYKFEDSCTWCNGTMATISSGEENDFYSRVFGSNDETTRQIWIGNT ESSGYLNWSQGQPTKPNDGLDYCISMDLSAGSTRGKYKYLPCQSTVINSLCYMNP * join (29612 . 29663, 29708 . 29817, 29871 . 29983, 30029 . 301
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/gene="F08G5.t1"
                                                                                                                                                                                                                                                            /protein_id="CAA94586.1"
/db_xref="GI:3875595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(29612. .2
30196. .30308,
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/db_xref="GI:3875594"
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/gene="F08G5.5
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/db_xref="GI:3875590"
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                                                                                                                                                                                                           /db_xref="SPTREMBL:Q19223"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )oin(29612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F08G5
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                                                2.1%; 68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .29663,
Score 44.6; DB 3;
Pred. No. 0.97;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                             8,30695. .31054,31781.
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4,31781. .31951)
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REFERENCE
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VERSION
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AF429315/c
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agggagtaattgggccgcaaaagggagtaattgggccgcaaaagggagtaattgggccga 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 125020)
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hw Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Bric Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmes, S.E., Inge
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                   Similarity
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="isolated from a patient
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                       /product="junctophilin 3"
complement(<36507. .>36887)
                                                                                                                                                      /product="junctophilin 3"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/db_xref="Gi:17646245"
/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
/translation="MSSGGRENFDDGGSYCGGWEDGKYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLODGYGTETYSGG
NGAKYEGTWSNGLODGYGTETYSGG
32731 c 30696 g 28283 t 4254 others
                                                                                                                                                                                                                                                                                                 membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_unit=ctg
complement(<3
                                                                                                                                                                                                                                                                                                                                                        complement(<36507. .36887)
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/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                              note="component of the junctional complex between
                                                                                                                                                                                                                                                                                                                                    /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                      /note="JP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="16q24.3; between D16S520 and WI-12410"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="16"
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junctophilin 3 (
                                                 %; Score 44.2; DB 9;
%; Pred. No. 1.6;
345; Mismatches 417;
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                                                                                                                                                                                                                                                                                                                   STRGSSAGKKSSYKKMSCCARYKSMS 16965
                                                                                                                                                                                                                                                                                                                                                  agacgacccaaccgtcgccaggcgcg 1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKYKCSWSSMYKCKTSKSYRRKRSYYYWGGGKRAKKKYYCAGRRRRMSYWKCCAKWWMSY 17591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acaagtggccgcagaccgggccttcgaccagacaaaaactgtgctccctgccgaggtggc 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cagatttgctctcaaacctgcactggatgagatcaaccatttatcgcgtctgacattgac 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgagttgcgggcgctccttggagtgcccgagggaaagatggttcgttggaacgacgttaa 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRSRAMMNGNAAAAGCTTCCCCANTNGGGGGAAAAAGGGCGSASRASCYKGRMSSKSCYR 17171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccagcacgtctctagtctcgccaatcttgatcggatgagcgcgaaaacctttacggtccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMKMYKSYYRRKRWMTCMKMCYSMYMAMYCRSMCCMCMCKSCCGCYSMGMSSYSYSGKYS
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovinae; Bos. 1 (bases 1 to 3490)
                                                                                                                  COW.
                                                                                                                                 Bos taurus mRNA for IkB
AJ414556
AJ414556.1 GI:15986410
bIKKbeta gene; IkB kinas
Rottenberg, S.,
                                                                                                Bos taurus
                                                                                                                                                                                                                   BTA414556
Dobbelaere, D.A.E.
                                                                                                                                     kinase-beta
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and
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  Heussler, V.T
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                                                                                                                                                                                                                                                                                                                                    tgtgcgccatgaaatgcggctggccgacattcgcgcaatcgacggcatgaaaaaccatga 725
                                                                                                                                                                                                                                                                                                                                                                         GCAGGCGCGGGAGCTTTACCGCAGGCTGAGGGGAGAGCCCAGAGACCCAGCGGACTGATGG 1789
                                                                                                                                                                      GCTGCCCAAGGTGGAGGAGGTGGTCAGCCTGATGAGCGAGGACGAGAAGATGGTGGTGCG
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                                                                                                                                                                                                                                        GCGAGTGATTTATACGCAGCTCAGTAAGACCGTGGTCTGCAAGCAGAAGGCCCCTGGAACT 1909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rottenberg,S.
Direct Submission
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 AE005932
Caulobacter crescentus
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DLRKYLNQFENCCGLREGAILTILSDLASALRYLHENRIIHRDLKFERIVLOQGEQRL
HKIIDIGGYAKELDQGSLCTSEVGTLQYLAPELLEQQKYTVTVDYWSFGTLAFECITG
RPFLPNWQPYQWHSKYRQKSEMDIVVSEDLNGAVKFSSSLHHPNNLMSVLAQRLEKW
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ARELYRLREKERDQRTDGDSQEMVRLLQALQGGFEKKVRVIYOLSKTVVCKQKALE
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/db_xref="taxon:9913"
/clone="plate 77, row E,
Animal Research Center"
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/function="Signalling molecule
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4 Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Nelson, W.C., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Berrolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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WIDAGSMMEADDOGGLAHFLEHMAFNGSKNV PEGEMIK LERHGLAFGADTNASTSFD
ET I YQLDLPKTDDDTVDTSLMLLREAGELTI APEAVDREERGVVLSEERTRUDFGYRV
AIKTLGAGMEGOLIPKE I PIGKTEVLKTAPAQRIRDFYEAY X REERTVLVAVGDFDVD
AIKTLGAGMEGOLIPKE I PIGKTEVLKTAPAQRIRDFYEAGAPWSIOMTWTRKEED
AMEAK I KGKFGDWVGKGPNGKDPDVGPVAKRGPTAKMFVEAGAPWSIOMTWTRKEEGL
LETKAVDERDTLENLGFAVLNRALGAVGRSAEPPF I AGGAFKGDOFGAVRVTTTFGATA
OPGRWREALTALDAEDGRAFA I GVGVVGNELDRELTASLRAGILVAAAAGEATGRTPSLANQ
LVGTLGDGEVVTSP SQNLAAFDLFVKGLTAERVNAVLKSAFVGSGPLLVLAAPTAVEG
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GEPATICAT SELLAGAFTLINGRTRPEDLSTELQVLAAFTEPGWRPEAFNIKTSTYGT
LTGK I WNAQLGVUGNDLGGLAHRAFGOLDFTLAGATAFTEPGWRPEAFNIKTSTYGT
LTGK I WNAQLGVUGNDLGGLAHRAFGOLDFTLAGATAFASTEPGWRPEAFNIKTSTYGT
LHDQLLGSTTGGVUGNDLGGLAHRAFGOLDPLPGAGKAPFTDEGWRPEAFNIKTSTYGT
LHDQLLGTTTURKAI LAAVADTFGALLPARFGOLDPLPGAGKAPFTDAGERVATATASVVFD
DAGYLAVSLEVPPEKLLOGVVASITK I AADLINGKFYSADELDLRAKKPR IDALEKARVTN
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/db_xref="Gi:13424217"
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/product="hypothetical
/protein_id="AAK24606...
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                  aı protein"
5.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shetty, J.,
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gene CDS

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/translation="MKAPKLNTRAWTIALGAMLGGLLLGGAAYAAGCTKACPPPPPVC
CRPPPPPKPPAPPTGCCGGGHWNIPGVNVNLGSTVIVNATTATATRATRTRTRV
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IVRAVCLDDRDVPHAASQVTPDREIDEAYDGELYRCIAGARLQYVIAEYGGHIDISTG
                                                                                                                                                                                                                                                                                                                                                                                                                                         GLGRQQFLESGAFLKSRPDLDRPDLQIHGVLAIMQDHGKVVVEKDGFTLHVCQLRPES
RGKVGLRSADPFDDPTILGNYLATEEDRRAIREGVRIARETVAQAAFDPYRDAEYAPG
ADVKSDADLDAWIRSKAETIYHPVGTCRMGVAGDPMAVVDDQLRVQGVQGLRVIDASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mrhrplgrsglltaplifggnvfgwtadeamshrlldafidggf
navptadvysawvpghaggesgavigrwlkasgkrdsylvltkvamwprapglsaani
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lkasllvstasglarvetiqpkfnlvdrdovegalaelanaegigiipyglaagelt
ekxpsegdlegrargrtilhdywndkgravlaaldeaaaavgaspaqvalawimrhps
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LELLPQVFVLGREGGKLPFRLAGGFVSDLHARDLRGHDALSLWALAHRLELKSALDVA
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3970. .4722
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TETYTAYREETVQERQTLSTSFSLDGGVGGVVY"
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ARGDNDPITIGENSNVQDGSVLHTDLGAPLTIGANVTIGHMVALHGCTIGDGSLIGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVEAGRQAGHKTTKDFNGYQQEGFGPYDLTIRDGQRWSAAMAYLNQALSRPNLTCVTE
ACTTRIILDKRRAVGVEYVVGKSREKQVAYADAEVLLSAGAVQSPQILQLSGIGAAED
LAPHGIAVAHESKGVGANLQDHLDVCVSWTAKNLKTAYSANKGLNKLGVGMNYMFFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKMPAGVGQLIKDKGEQNWGFWTEAEPHLDNRKLWWPRGKGLGGSSAINGMIYIRGH
ARDYDQWRQMGLTGWSYSEVLPYFKRSETHHAGGDAYHGGSGPLHVSKGESDSPFYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITAPIASATTVEQLDDLMGAARLDLPDDIWATLDAAGR"complement(5674...7341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKRRTPVVVTADIRAHGVPSVGMEVLFAPLQGASGETDRELGLYQPIAMTARLMGRPA
YELGLEREIK PLGDGNQDMPRLKLATLDGRRIA"
Complement (4719. . 5663)
/gene="CC2641"
                                                                                                                                                                                                                                                                                                                complement(7633. .8163)
                                                                                                                                                                                                                                                                                                                                           complement(7633.
/gene="CC2643"
                                                                                                                                                                                                                                                                                                                                                                                                              MPTLIGGNTNAPTIMIAERAADLIRGKTPAAPLDVPVYEDGRAVAAE*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_1d="AAK24609.1"
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/translation="MASERFDYIVIGAGSAGCVLAARLTEDPNIKVLLLEAGGKNKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="choline dehydrogenase"
/protein_id="AAK24609.1"
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/protein_id="AAK24608.1"
/db_xref="GI:13424220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/trans1_table=11
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SIVLNGAKIGKNCLIGAGALITEGKEIPDNSMVMGAPGKVVREIGEQHAMILQASALH
                                                                                                                                                                                                                                                                           /gene="CC2643"
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AG 11589
                                     ag
                                                                                                                                                           TGCGCAAGACCAGCCACGAGCGCCTCAGCCTGCCGCCGCTGGGCGTGGGCCTGGCCGATCT 11527
                                                                                                                                                                                             acggcatgaaaaaccatgaccgtgagagcctgaccccgctgttcgaggagctagccgctg
                                                                                                                                                                                                                                                                gcggccgcatggctgatgatgtgcgccatgaaatgcggctggccgacattcgcgcaatcg 706
                                                                             cggtgttgacccatgatgaccctgcaaagatgatcgtgacagtcggcggcttggtcgatg
                                                                                                                                                                                                                                       GGGGCCTGTTGGGCTATGGTGCCCTGATCGGCCTGGGCCTGGTCGCCCGTCGACGCGATCC 11467
                                                                                                                                                                                                                                                                                                                     l Similarity
95; Conserv
                                     828
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMGITVGVAMFTGLFIAWAILVPILTLVTPMPEADAATHALTVWKSQVRFLGAGVIGA
AAIWTLAKLVGPITSGLKSAFAAAQARKAGGAKLPVEDDIPIGIVGLVSVLLLAPAG
WFLAHFLTGGPIASLTTPLVAIGIGYLVFAGLILAAAVCGYMAGLIGSSUSPVSGIAIL
SVLGASLMVGHVGGGVLGPDVTKALIAFALYVTTCVLLAVAVVANDNLQDLKTGQLVDA
TPWKQQVGLIIGVLAGSMVIPFVLELLNRSYGFAGAPNLQAISDEPLAAPQATLISTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="oligopeptide transporter, OPT family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSLIKSAFLATTLLALAASPVSAEQFVVPQSSAGTMSQIDLWGR
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9853. 11853
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8525. .9277
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/note="identified
TIGR00733"
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Ylktikgegqqlweaideknlymalgagtgkytaliskatleagrysrtyls
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RGRTLNNAFVVIDEAQNCTYMQLKMLLTRLGWHSTMVVTGDPNQSDLLPGISGLAEVA
                                                                                                                                                                                                                                                                                                                                                                                                     PLALPFAPSEHVGMFLSLAAAAIVVVGFYRWARKAGAKAMEA" 11860. .12507
                                                                                                                                                                                                                                                                                                                                                                                                                                          AKGVLGGNLDWGLLGYGALIGLGLVAVDAILRKTSHERLSLPPLGVGLAIYLPSSVTA
PVVVGALAGWLYEKVVSKDRAAEPSRRLGVLIASGFIVGESLFNVSLALLIVSTGKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPTFGACAVGGILGVMYTIPLRRALVTNSNLPYPEGVAAAEVLKVGAGSREGAAEGKA
GLAAIGFSALASALFGALGAAKLFAAEIAAYFKFKLGAASGATGIGASSSLALMGAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CC2646"
9853. .11853
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/protein_id="AAK24612...
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9453...9758
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/transl_table=11
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PID:1651507; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:1651507;
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/db_xref="GI:13424223"
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Pred. No. 2.7;
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DEFINITION
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AUTHORS
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 158
                                                           218 NMWWVKCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRMAHHHWCATNNNMMWWWYAYMH
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Sequence 22 from Patent WO0111061.
AX083744
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/db_xref="taxon:32630"
1. .1141
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a 32 c 42 g 112 t 832 others
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Search completed: August 20, 2002, 16:27:03 Job time: 11466 sec

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ALIGNMENTS

RESULT AAS18306

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Cloning vector; Ketogulonigenium replicon; endogenous plasmid: transformed host cell; Escherichia coli; pADM291; ds. D'Elia AAS18306; AAS18306 standard; DNA; 2112 (ARCH) ARCHER-DANIELS MIDLAND (DELI/) D'ELIA J. 05-APR-2000; 2000US-194625P 05-APR-2001; 18-OCT-2001 WO200177347-A2 Ketogulonigenium sp. strain ADM291-19 DNA sequence of Ketogulonigenium replicon from plasmid pADM291 12-MAR-2002 (first entry) 2001WO-US11059 ВP co

Novel nucleic acid vector comprising Ketogulonigenium replicon a specific deposited endogenous plasmid, useful for producing

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WPI; 2002-049150/06

host cells transformed

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                      The present invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, paDM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coli, enable the cloning of certain genes of Ketogulonigenium in E.coli as the latter is an efficient host for amplification of vector DNA. The present DNA sequence represents the
                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid vector comprising Ketogulonigenium replicon found a specific deposited endogenous plasmid, useful for producing polypeptides and/or transcripts by culturing host cells transformed with vector -
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                                                                                                                                                                                                      The present invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, pADM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coll, enable the cloning of certain genes of ambification of vector DNA. The present DNA sequence represents the amplification of vector DNA. The present DNA sequence represents the region of Ketogulonigenium endogenous plasmid pADM291 that supports plasmid vector replication.
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AAI67035;

AAI67035 standard; DNA; 8509 ВР

RESULT
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XX AA16
XX AA16
XX Il-F
DT 11-F
DE Nucl
XX Vetc
XX Synt
XX Synt
XX Synt
XX W020
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Ketogulonigenium; plasmid; strain NRRL ketogulonigenium в-30035; plasmid

S X C C C C C C C C X S X X P P T X X P P X X F F X X F F T X X P P T X X P P T X X P P T X X P P T X X P P T X X P X X P T X X P X X P T X X P X X P T X X P X

Claim

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Query Match
Best Local
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           The invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, pADM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coli, enable the cloning of certain genes of Ketogulonigenium in E.coli as the latter is an efficient host for amplification of vector DNA. The present DNA sequence represents the Ketogulonigenium endogenous plasmid pADM291.
                                                                                                                                                                                 Novel nucleic acid vector comprising Ketogulonigenium a specific deposited endogenous plasmid, useful for pr polypeptides and/or transcripts by culturing host cell with vector -
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RESULT AAQ21036 ID AAQ2

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Matches 104; Conservative
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Note: The sequence data for this patent did not form part
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novel human diagnostic protein #17600
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed at the print
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
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                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic;
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,\,
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                                                                                                                           acgaaaattacacataattatcaatagcttattcgcttaaaagggagtaattgggccgca
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larity 57.7%;
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antianaemic; cytostatic; nootropic;
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06-NOV-2000; 17-MAY-2001.

2000WO-AU01362

(META-) METABOLIC 05-NOV-1999;

PHARM LTD

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Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism; modulation; lipolysis stimulation; hormone-sensitive lipase stimulation; lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity; functional food; transgenic yeast; fat/lean ratio; food use; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC organisms comprise a polynucleotide encoding a growth hormone fragment CC capable of stimulating the activity of hormone-sensitive lipase (the key CC enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key CC enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key CC enzyme in lipolysis). The growth hormone fragment preferably contains CC at least the disulphide-bonded loop of a mammalian growth hormone (but is CC not the full-length growth hormone) and is optionally linked to an CC epitope tag or heterologous fusion protein partner. The transgenic CC organism may be a microorganism used to produce a fermented product CC (e.g., yeast), or an edible plant or animal or cell thereof. Food or CC drink made using methods of the invention are used to modify fatylean CC ratio, lipid metabolism or food use in a mammal. In particular, the food CC or drink products may be used to treat or prevent obesity, particularly CC in humans, and may also be used to improve the fatylean ration of the CC invention, the human growth hormone (hdf) fragment analogue AOD9604 was CC expressed in yeast, optionally fused to the FLAG epitope (AAB73625). CC The present sequence is described as a DNA sequence from yeast in CC expressed in the sequence listing, but is not further referred to in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                           RKKHKAGHMSRHNWKDSVKATKY 3823
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                                                                                                                                                                                                                                                                                              BBKMCHVTDGANDHDHDHGANDNDNNDKDKDCYNKRRBHHHDHDHDBYVNDNDGWHND
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AAS87283 standard; cDNA;

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                                                                                                                                                                                                                                                                                                                                          (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                          1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS87283;
                            429
956
                                                                                        369
                                                                                                                                 Local
                 cgcaaaagggagtaattgggccg
                                                          ACACAGGAGTATTGGGGATGCACACAGGAGTATTGGGGATGCACATAGGAGCACTGGGGA
                                                                          2001-639362/73
TGCACATAGGAGTATTGGGGACG
                                                                                                                    l Similarity
55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG23096
                                                                                                                                                                                               2047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0540217
2000US-0649167
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                                                                                                                                                                                               BP;
                                                                                                                                                                                               402 A; 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23087; 103pp;
                                                                                                                                   1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΥŦ
                                                                                                                    0;
                                                                                                                                   Score
Pred.
                            451
                                                                                                                                                                                               c;
                                                                                                                    Mismatches
                                                                                                                                                                                               589
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                                                                                                                                   38.2;
No. 0.
                                                                                                                                                                                               ე.
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                                                                                                                                                                                               441
                                                                                                                                   .73;
                                                                                                                                                                                               T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #23087
                                                                                                                    28;
                                                                                                                                                  23;
                                                                                                                                                                                               0 other;
                                                                                                                    Indels
                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forensic;
                                                                                                                                                  2047;
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RESULT 13
AAS17226
ID AAS172:
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AC AAS172
XX
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                                                                                                                                                                                                                        В
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                                                                                                             밁
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Conserv
                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new bacterium of genus Ketogulonigenium. Ketogulonigenium may further comprise a transgene, comprising a DNA sequence from an endogenous ketogulonigenium plasmid. Methods for transforming Ketogulonigenium are also described. The invention is useful for producing 2-keto-L-gulonic acid (2-KLG) from L-sorbose or sorbitol. The present sequence represents the nucleotide sequence of replicon #1 on the Ketogulonigenium endogenous plasmid pADDMX6L1. Note: The present sequence for SEQ ID No 5 given in Fig 5 is different that given for SEQ ID No 5 in the sequence listing (AAS17226).
                                                                                                             1104
                                                                                                                                       1723
                                                                                                                                                                    1044
                                                                                                                                                                                                1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Fig 5; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bacterium of Ketogulonigenium genus, useful for producing 2-keto-L-gulonic acid from sorbose or sorbitol, comprises transgene containing DNA sequence from endogenous Ketogulonigenium plasmid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D'Elia J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ketogulonigenium robustrum strain pADMX6L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ketogulonigenium; 2-keto-L-gulonic acid; L-sorbose; sorbitol;
plasmid replicon pADMX6L1; replicon; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Replicon sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS17123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS17123 standard;
                                                                                                                                                                                                                                         1603 aggctgcaaaagcaacgggtgtggcgaccgcaaccatcactcgggcgctaaaaaagcggta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARCH ) ARCHER-DANIELS MIDLAND (DELI/) D'ELIA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000US-194627P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2001
               AAS17226;
                                                                                                                                                                                                                                                                                                                                                 Sequence 1456 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STOD/) STODDARD S F.
                                         AAS17226 standard;
                                                                                                                                                                                                                          984
                                                                                                                            gagtgtttcctccca 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-041295/05
                                                                                                                                                                 agatttcaggtgttcaggatggacaaggaacgtggacaatagacccctcagagatggcaa
                                                                                                                                                                                             aaatttccggtaaaaaagatgaatctggggcatgggttatagatcctgcagaattgcaca
                                                                                                                                                                                                                        aggcggtaaaacacttcgatgtttcccggccaaccctgcaaaaagcccttaaatctggca
                                                                                                            gagtttaccagccaa 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replicon
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pADMX6L1; replicon;
                                                                                                                                                                                                                                                                                                                                                364 A; 423 C; 415 G; 254 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #1 of Ketogulonigenium endogenous plasmid pADMX6L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SF;
                                                                                                                                                                                                                                                                                           1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1456
                                           1458
                                                                                                                                                                                                                                                                              ; Score 37.4; D
; Pred. No. 1.1;
0; Mismatches
                                           ВP
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                                                                                                                                                                                                                                                                                                         BB
                                                                                                                                                                                                                                                                                61;
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                                                                                                                                                                                                                                                                                                          Length 1456;
                                                                                                                                                                                                                                                                                                                                                                             5 is different (AAS17226).
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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                              1722
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RESULT 14
AAS17119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ωy
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ketogulonigenium plasmid. Methods for transforming Ketogulonigenium are also described. The invention is useful for producing 2-keto-1-gulonic acid (2-KLG) from L-sorbose or sorbitol. The present sequence represents the nucleotide sequence of replicon #2 on the Ketogulonigenium endogenous plasmid pADMX6L1. Note: The present sequence for SEQ ID No 5 given in the sequence listing is different from that given for SEQ ID No 5 in Fig 5 (AAS17123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1603 aggctgcaaaagcaacgggtgtggcgaaccgcaaccatcactcgggcgctaaaaagcggta 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new bacterium of genu Ketogulonigenium. Ketogulonigenium may further comprise transgene, comprising a DNA sequence from an endogenous Ketogulonigenium plasmid. Methods for transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bacterium of Ketogulonigenium genus, useful for producing 2-keto-L-gulonic acid from sorbose or sorbitol, comprises transgene containing DNA sequence from endogenous Ketogulonigenium plasmid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200177348-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ketogulonigenium
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                                                                                                                                                                                                                                                                                                                                             AAS17119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1106 gagtttaccagccaa 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1723 gagtgtttcctcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 97; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STOD/) STODDARD S F.
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                                         Ketogulonigenium
                                                                                                                                            12-MAR-2002
                                                                                                                                                                                                                                               AAS17119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaatttccggtaaaaaagatgaatctggggcatgggttatagatcctgcagaattgcaca 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-041295/05
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                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                            (first entry)
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                                         endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-keto-L-gulonic acid; L-sorbose; pADMX6L1; replicon; ds.
                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
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Pred. No. 1.1;
0; Mismatches
                                    plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                              pADMX6L1
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                                                    DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a new bacterium of genus Ketogulonigenium. Ketogulonigenium may further comprise a transgene, comprising a DNA sequence from an endogenous Ketogulonigenium plasmid. Methods for transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bacterium of Ketogulonigenium genus, useful for producing 2-keto-L-gulonic acid from sorbose or sorbitol, comprises transgene containing DNA sequence from endogenous Ketogulonigenium plasmid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D'Elia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                           2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Fig 1; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ketogulonigenium robustrum strain ADMX6L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ketogulonigenium;
plasmid pADMX6L1;
 13-FEB-2002
                         AAS54178;
                                                AAS54178 standard; DNA; 858
                                                                                                                                                                                                                                                                                                                     Sequence 7029
                                                                                                                                                                                                                                                                                                                                                                 Ketogulonigenium are also described. The invention is useful producing 2-keto-L-gulonic acid (2-KLG) from L-sorbose or so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STOD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ARCH ) ARCHER-DANIELS MIDLAND CO. (DELI/) D'ELIA J.
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                                                                        15
                                                                                                                                                                                                                                                                                                                                                      present sequence represents Ketogulonigenium endogenous
                                                                                                                                                                      aaatttccggtaaaaaagatgaatctggggcatgggttatagatcctgcagaattgcaca 1722
                                                                                                                                  gagtgtttcctccca 1737
                                                                                                                                                                                                        aggcggtaaaacacttcgatgtttcccggccaaccctgcaaaaagcccttaaatctggca
                                                                                                          gagtttaccagccaa
                                                                                                                                                        agatttcaggtgttcaggatggacaaggaacgtggacaatagacccctcagagatggcaa
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1755..3210
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                                                                                                                                                                                                                                                                                                                     1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "pADMX6L1 replicon, corresponds to AAS17123"
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                                                                                                                                                                                                                            cc genes, their use in the discovery of novel antiblottics, the essential cc genes themselves and the encoded proteins. The prokaryotes used are cc Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella cc pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The cc invention is also useful for the identification of potential new targets cf or antiblotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. cc and to obtain antibodies capable of binding to the expressed proteins. cT he proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen cor homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000;
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                                                                                                                                                                                                                         Sequence
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P-PSDB; AAU36319.
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26-MAY-2000;
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                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
           802
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                                                                                                                                                   Local Similarity 43.0 nes 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides for the identification and development ibiotics, comprise sequences of antisense nucleic acids
gtgacagtcggcggcttggtcgatgaggcgcgaatagactaccgccaggaggcaagcggc
                                     gcgttggtcgaccagcagtccttctatgtggtcgcctacttcgaggaaaccaagctgccc
                                                     ccgctgttcgaggagctagccgctgcgggtgttgacccatgatgaccctgcaaagatgatc
                                                                                             caggtaaccaacctgcgcctggcccagggcaactacgccacggcgggccaggcggtgatg
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; antibacterial;
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2000US-206848P.
2000US-20772PP.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                                                                                                                          BP; 149
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Xu HH;
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re greater than or equal to the score of the result being printed,
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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4 US-09-007-005-17
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4 US-09-103-840A-1
3 US-09-141-000-2
4 US-09-182-024A-1
US-09-182-024A-1
2 US-08-486-839-3
3 US-09-151-011-3
4 US-09-343-623-3
4 US-09-151-011-5
4 US-08-187-793-1
1 US-08-187-793-1
1 US-08-187-793-3
1 US-08-453-624-94
1 US-08-453-624-94
1 US-08-453-702A-94
2 US-08-453-702A-94
4 US-08-93-12588-94
5 PCT-US93-12588-94
                                  US-07-998-003A-102
US-08-453-274B-102
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Sequence 14, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 94, Appl
Sequence 9102, App
Sequence 102, App
Sequence 102, App
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1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6
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Sequence 1, Ap	Sequence 2, Ap	Sequence 1, A	Sequence 1, A	Sequence 1, Ap	Sequence 1, Ap	Sequence 1, Ap	Sequence 1, Ap	Sequence 10, 1	Sequence 1, Ap	Sequence 1, A	Sequence 3, Ap	Sequence 3, Ap	Sequence 102,	Sequence 102,	Sequence 102,	Sequence 102,	Sequence 102,

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ALIGNMENTS

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RESULT 1 US-08-232-463-14/c US-08-232-463-14/c Sequence 14, Application US/08232463 Patent No. 5670367
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                               TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNUER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE DATAGE FARTMENT
                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114
TELECOMMUNICATION INFORMATION:
                                                               TOPOLOGY: 11
                                                                                                                                                                                                     TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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1800 Diagonal Road,
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                                                                                single
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Query Match Best Local Matches

Local Similarity

2.2%; So illarity 3.8%; Proceed to Conservative 205;

Score 45.8; DB 1; Pred. No. 0.00022;

Length 7218; Indels

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Gaps

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Mismatches 152;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                        NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1594 cggctggacaggctgcaaaagcaacgggtgtgggcgaccgcaaccatcactcgggcgctaa 1653
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INFORMATION
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                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1097 RRRRRRRRRR 1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                             APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
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   SEQ ID NO:
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SELECTION OF PROTEINS USI
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION UNMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION UNMBER: 60/035,963
EARLIER APPLICATION UNMBER: 60/035,963
EARLIER APPLICATION UNMBER: 60/064,491
EARLIER FILING DATE: 1997-01-06
EARLIER FILING DATE: 1997-11-06
NUMBER: 07 SEQ ID NOS: 33
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Best Local S
Matches 26
                                                                                                                   ; LOCATION: (1)...(289)
; OTHER INFORMATION: n
US-09-007-005-17
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              QУ
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APPLICANT: SZOSTŁAK, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                     SEQ ID NO 17
LENGTH: 289
                                         Best Local Similarity
Matches 14; Conserv
                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Translation
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          TYPE: RNA
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                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                             FEATURE:
351 tcaatagcttattcgcttaaaagggagtaattgggccgc
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TOPOLOGY: li
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                                                            1.7%;
                                                                                                                                       = A,T,C
                                               %; Score 36; DB;
; Pred. No. 0.042
93; Mismatches
                                                                                                                                                                                                  template
                                                                  DB 4;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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RESULT 5
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
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US-09-244-796-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007 CURRENT APPLICATION NUMBER: US/09/244,796 CURRENT FILING DATE: 1999-02-05 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27 EARLIER FILING DATE: 1997-01-27 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06 EARLIER FILING DATE: 1997-11-06 EARLIER FILING DATE: 1998-01-14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Translation template FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                rnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrs 200
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6.4%; Pred. No. 0.042;
htive 93; Mismatches 113; Indels
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US-09-103-840A-1/c
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US-09-103-840A-1
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SEQ ID NO 2
                                                                                                                SOFTWARE: PatentIn
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09103840A Patent No. 6294328
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M.
                                                                                                                                                            FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                      APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4403765
TYPE: DNA
                                                                                          LENGTH: 4411529
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Pred. No. 37;
0; Mismatches 102;
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Query Match
Best Local Similarity
Matches 97; Conserv

1.7%; Score 35.8; 48.7%; Pred. No. 3

0;

Mismatches

Indels

0;

Gaps

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37; DB 4; 37; ches 102;

Length 4411529;

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US-09-141-000-2
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; ORGANISM: Human
US-09-141-000-2
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CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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APPLICANT: Chen, Fang
APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
FILE REFERENCE: 19999Y
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Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                  134 NIEYSCPATNECEITKRRRKSCOACRFMKCLKVGMLKEGVRLDRVRGGRQKYKRRLDSES
                                                                                                                                       314 LAGLLELYRAILQLVRRYKKLKVEKEEFVTLKALALANSDSMYIEDLEAVQKLQDLLHEA 373
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nes 40; Conserv
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                               acgctgcaaacatcgaaaaactgtttttagatttctgcgcaaaggtagggaaggtttgag
                                                                  LQDYELSQRHEEPWRTGKLLLTLPLLRQTAAKAVQHFYSVKLQGKVPMHKLFLEMLEAKA 433
                                                                                                IIGWAKHIPGFSSLSLGDQMSLLQSAWMEILILGIVYRSLPYDDKLVYAEDYIMDEEHSR 313
                                                                                                                                                                                                                                                                                SPYLSLQISPPAKKPLTKIVSYLLVAEPDKLYAMPPPGMPEGDIKALTTLCDLADRELVV
WARADSLQEWRPLEQVPSPLHRATKRQHVHFLTPLPPPPSVAWVGTAQAGYHLEVFLPQR 493
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8.2%; Pred. No. 0.22;
ative 141; Mismatches
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PRIOR APPLICATION NUMBER: 60/06.
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/09.
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1.
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US-09-182-024A-1/c
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Connoll APPLICANT: Rajput,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09182024A Patent No. 6342370
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                            Sequence 3, Application Patent No. 5928928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Description of Artificial Sequence:cDNA coding OTHER INFORMATION: the human slit polypeptide of SEQ ID NO:2
                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                           TITLE OF INVENTION: IN NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                             APPLICANT
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                                                                              STREET:
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                              STATE: New York COUNTRY: United States of America ZIP: 11758
                                                                                                               ADDRESSEE:
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                                                                                            Hoffmann & Baron
00 Jericho Turnpike
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                                                                                                                                                                                                                                                               US/08486839
     disk
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08 FILING DATE: 07 - June - ATTORNEY/AGENT INFORMATION: NAME: Baron, Ronald J.
                            APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
NAME: MOILLS, ROBERT C.
REGISTRATION NUMBER: 42,910
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1488
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HYPOTHETICAL:
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TITLE OF INVENTION:
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                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING
                  REFERENCE/DOCKET NUMBER:
                                                                                                                                       SOFTWARE
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                             STREET:
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                           42,910
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                  294-32 DIV
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Pred. No. 0.62;
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RESULT 11
US-09-343-623-3/c
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (516) 822-3582 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                      TELEFAX: (516) 822-358
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                        REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Baron, Ronald J.
                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 07-June-1995
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
           TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                         NAME: Baron, Ronald REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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 TOPOLOGY:
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350 Jericho Turnpike
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Best Local S
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                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                     TELEPHONE: (516) 822-3550
TELEPHONE: (516) 822-3582
TNFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              NAME: Barron, Ronald J.
REGISTATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 29.
TELECOMMUNICATION INFORMATION:
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FILING DATE: 07 - June -
ATTORNEY/AGENT INFORMATION:
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1146 tttatcgcgtctgacattgacggcaaagccgaccaagattggccgtagcgtagcgaggtgt 1205
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hes 78; Conserv
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CITY: Jericho
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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350 Jericho Turnpike
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                                                            Conservative
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51.7%;
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in therapy or prophylaxis against infection
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                                                          Score 34.2; DB Pred. No. 0.64; 0; Mismatches
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US-09-151-011-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PTITLE OF INVENTION: TITLE OF INVENTION: TOUR OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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 CAGGAAAACCCAGGAGGCAGGCTGTAGAGTG 1529
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6900 Jericho Turnpike
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US-09-343-623-5/c; Sequence 5, App.

Application US/09343623

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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                     GENERAL INFORMATION: APPLICANT: POSNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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HYPOTHETICAL:
                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                               APPLICANT: POSNER, JEROME B.
APPLICANT: DARNELL, ROBERT B.
APPLICANT: FURNEAUX, HENRY M.
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 07-June-1995
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CURRENT APPLICATION DATA:
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ADDRESSEE: Hoffmann & Baron
 NUMBER
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CITY: Jericho
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ZIP: 11758
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SEQUENCES:
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51.7%;
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                ANTIGEN RECOGNIZED BY ANTIBODIES ASSOCIATED WITH PARANEOPLASTIC OPSOCIONUS AND METHODS OUSE THEREOF
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TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEFAX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                                                                                                                                                         Matches
                                                                                                                                            1595
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APPLICATION NUMBER: US 691,559
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: D
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39
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CITY: NEW YORK
STATE: NEW YOR
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OTHER INFORMATION:
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ZIP: 10112
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1: em
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F.,
Nagai, M.A., da Silva, W. Jr., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMI-NN1200-151200-013-h06 NN1200 Homo sapiens cDNA, mRNA sequence
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                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=pMl&t2=pMl-NN1200-
151200-013-h06&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
seq primer: puc 18 forward
                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                           Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                      sequence tags
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                                                                                                                                                                       Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7t1=MR3&t2=MR3-NN0219-
081200-012-f10&t5=2000-12-08&t4-1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                             High quality sequence start: 30 High quality sequence stop: 303 Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
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as Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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/db_xref="taxon:9606"
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                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0219"
                /dev_stage="Adult"
    /note="Organ:
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78.6%;
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AGCATTTCCTTCTGGTCCAGCCTCTCCGTCTTGTCCAGCTTGTCCTGGTTGTCCGTCTGG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biology Lab.
National Institute of Genetics
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Expression map of the C.elegans genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
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                                                                     h 2.18;
Similarity 68.18;
62; Conservative
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81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                       ykohara@lab.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                /clone_lib="Yuji Kohara unpublished cDNA"/sex="hermaphrodite, male"/tissue_type="whole animal"/dev_stage="varied"/dev_stage="varied"/1 t
                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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61.2%;
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                                                                     Score 44.6; DB Pred. No. 0.11; 0; Mismatches
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                                                                                                                                                    l Similarity
54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESD/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-MR3&t2-MR3-NN0219-
281000-004-804&t3-2000-10-28&t4-1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MR3-NN0219-281000-004-a04 NN0219 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
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/dev_stage="Adult"
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Pred. No. 0.13
0; Mismatches
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MR3-NN0219-281000-006-g11 NN0219
BF947371
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Brunstein,A., deOliveira,R.R., Reis,L.F., de Souza,S.J. and
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF947371.1 GI:12364646
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-MR3st2=MR3-NN0219-
281000-006-gl1&t3=2000-10-28&t4=1)
Seq primer: puc 18 forward
High Canaltan Canalt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
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                                                                AW497369
392 bp mRNA linear ES ga59a02.yl moss EST library PPU Physcomitrella patens PPE SOURCE_ID:PPU090903 5', mRNA sequence.
AM497369
                                 AW497369.1 GI:7067514
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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pred. No. 0.15;
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Homo sapiens cDNA, mRNA sequence.
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Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Punariidae; Funariales; Funariaceae; Physcomitrella.

Bryopsida; Punariidae; Funariales; Funariaceae; Physcomitrella.

Bryopsida; Punariidae; Funariales; Funariaceae; Physcomitrella.

Eryopsida; Punariidae; Funariales; Funariaceae; Physcomitrella.

Contacts. Bashiardes,S., Cove,D., Cuming,A., Knight,C., Clifton (S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood (S., Marra,M., Hillier,L., Pape,D., Martin,B., Swaller,T., Underwood (S., Marra,M., Hillier,L., Pape,D., Martin,B., Swaller,T., Underwood (S., Marra,M., Hillier,L., Pape,D., Martin,B., Swaller,T., McCann,R., K., Thetsing,B., Allen,M., Bowers,Y., Person,B., Swaller,T., McCann,R., Waterston,R. and Wilson,R., Bowers,Y., Person,B., Swaller,T., McCann,R., Waterston,R. and Wilson,R., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R., Ritter,E., Jackson,Y., McCann,R., Leeds,Wash Undoss EST Project

Leeds,Wash Undoss EST Project

Washington University School of Medicine

Washington University School of Medicine

Washington University School of Medicine

Washington University School of Medicine
                                                                194 ttctgcctgtcgggcttgtcgggcttgtcggggcttgtcggggcttgtcggggcttgtcgggcttgtcgggcttgtcgggcttgtcgggcttgtcggggcttgtcggggcttgtcggggctgtccctc 253
217 recriteries estrected conference of the conf
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Location/Qualifiers
                                                                                                                                                                                                                                                             Similarity 73.
56; Conservative
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314 286 1810
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//note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="vector: pBluescript SK-; Site_1: CDNA
was carried out
xhor; Construction of the cDNA synthesis kit'. CDNA
using Strateagenes 'UnizAp - cDNA synthesis kit'. CDNA
contains a xhor site within it. Following ds cDNA
contains a xhor site within it. Following ds cDNA
contains a xhor site within it. Following ds cDNA
synthesis, EcoRI adapters were ligated to the blunt ends
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end on the other. This cDNA was ligated directionally in
end on the other. This cDNA was ligated directionally in
pBluescript sequence. The vector was
cloned within this pBluescript sequence. The vector was
cloned within this pBluescript and amplified. The library
was grown in XIIBlue MRF' cells and amplified. The library
was grown in XIIBlue MRF' cells and amplified. The library
was grown in XIIBlue was excision using Stratagens 'Mass
was excised by mass excision using Stratagens 'Mass
was excised by mass excision using Stratagens 'Mass
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single stranded plasmids that are then packaged (by helper
was plated out on LB-amp plates to select for
was plated out on LB-amp plates to select for
was plated out on LB-amp plates to select for
recovered. The double stranded plasmid library was
and recovered. The double stranded plasmid library was
and recovered. The double stranded plasmid library was
and recovered with pagen kit. 2 micro grams of
electroporation."

130 a 78 c 115 g 68 t 1 others
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/clone_1ib="Moss EST library PPU"
/tissue_type="protonemata: 7 day old tissue ammonium_grown"
/lab_host="DH10B"
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/db_xref="taxon:3218"
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                                                                                                                                                                                                                                                                   Score 44; DB 9;
Pred. No. 0.22;
0; Mismatches
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RESULT 8
BJ204205/c
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BJ183869/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo
excised from a modified IPs phage vector (Mo bi Tec, Germany). XhoI
digested-5' end of cDNA is ligated to SalI site of the vector, and
the BanHI digested-3' end including poly-A tail is ligated to BanHI
site of the vector. cDNA instert could be amplified with
conventional T7 and T3 primers. This normarized full- length cDNA
library was generated basically according to the method described
in Genome Research 10, 1617-1630 (2000), Carninci, P. et al.
Protonemata were blended by the POLYTRON, and then cultivated on
the BCD medium containing lum NAA (naphthalene acetic acid) for 8
to 11 days under the continuous light.
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Gaulonemata and rhizoid-like protonemata Physcomitrella pat subsp. pattens cDNA clone pphn50b12 5', mRNA seguence.
BJ204205
  вJ183869
вJ183869
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Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funaridae; Funariales; Funariaceae; Physcomitrella.
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, Carninci,P., Hayashizaki,Y.,
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
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                                                                                                                                                                                                                                                                                                                Similarity
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501 bp mRNA linear EST 24-normalized full length cDNA library, chloronemata
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pphn50b12"
/clone_lib="normalized full length cDNA library,
cchloronemata, caulonemata and rhizoid-like protonemata"
/tissue_type="mixture of chloronemata, caulonemata and
rhizoid-like protonemata"
105 c 150 g 93 t
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/db_xref="taxon:145481"
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                                                                                                                                                                                                                                                                                                              2.1%;
73.7%;
                                                                                                                                                                                                                                                                                           Score 44; DB 10;
Pred. No. 0.25;
D; Mismatches 20
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                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                    Length 497;
                       EST 24-JAN-2002
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A backbone of the vector is pBluescript II, that was in vivo excised from a modified IPS phage vector (Mo bi Tec, Germany). XhoI digested:5 end of cDNA is ligated to Sall site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This normarized full-length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 0.5MM BA (benzylaminopurine) for 8 to 13 days under the continuous light.
                   Physcomitrella patens subsp. patens. Physcomitrella patens subsp. patens sukaryota; Viridiplantae; Streptophy
                                                                                                                 BJ179016 TRIAN 11r
BJ179016 normalized full length cDNA library,
caulonemata and malformed buds Physcomitrella
cDNA clone pphb24104 5', mRNA sequence.
BJ179016
BJ179016.1 GI:18346970
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Fujita, T., Shin-i, T., Seki, M.,
Carninci, P., Hayashizaki, Y.,
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Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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  Eukaryota;
Bryopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/db_xref="taxon:145481"
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Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Funariidae; Funariales; Funariaceae; Physcomitrella.
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Shinozaki, K.,
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K., Kohara,Y.
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A backbone of the vector is pBluescript II, that was in vivo
A backbone of the vector is pBluescript II, that was in vivo
A backbone of the vector is pBluescript II, that was in vivo
A backbone of the vector is pBluescript II, that was in vivo
A backbone of the vector is pBluescript II, that was in vivo
A backbone of cDNA is ligated to Sall site of the vector, and
the BamHI digested-3' end including poly-A tail is ligated to BamHI
site of the vector. CDNA instert could be amplified with
conventional T7 and T3 primers. This normarized full-length cDNA
library was generated basically according to the method described
in Genome Research 10, 1617-1650 (2000), Carninci, P. et al.
Protonemata were blended by the POLYTRON, and then cultivated on
the BCD medium containing 0.5um BA (benzylaminopurine) for 8 to 13
days under the continuous light.
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Fujita, T., Shin-i, T
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Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                 subsp. patens cDNA cLone
BJ197576
BJ197576.1 GI:18365499
EST.
                  Unpublished (2002)
Contact: Tadasu Sh
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56; Conservative
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Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
                                                                      plants genome
                                                                                              Comparison of the moss Physcomitrella
                                                                                                                                              ıjita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
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/clone_lib="normalized full length cDNA library,
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and malformed buds"
/tissue_type="mixture of chloronemata, caulonema
malformed buds"
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Shin-i,T.,
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Tadasu Shin-i
or Genetic Res
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73.7%;
Resource
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Pred. No. 0.
  Information
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ches 20; Indels
                                                                                                   patens genome with flowering
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FEATURES
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PM1-NN1200-190201-018-h03 NN1200
BI033579
                                                                                                                                                                                                                                                                                                     Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D.H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                           Fax: +55-11-2707003
                                                                Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This sequence was derived from
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                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 97 (7),
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Tel:
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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ENTHS57TF Entamoeba histolytica
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Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
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301 838 3543
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/db_xref="taxon:9606"
/clone_lib="NN1200"
/dev_stage="Adult"
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/db_xreff"taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed
/note="Vector: pHOS1; Site_1: Bst I; Constructed
/note="Vector: phosphore in the property of the phosphore in the
                                                                                                                                                                     /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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JOURNAL MEDLINE REFERENCE MEDLINE REFERENCE RESULT 14 CNS07CVP/c REFERENCE SOURCE ORGANISM ACCESSION DEFINITION BASE COUNT AUTHORS TITLE Matches Query Match Best Local 9 AUTHORS JOURNAI AUTHORS JOURNAL 427 gccgcaaaagggagtaattg 446 212 367 ttaaaagggagtaattgggccgcaaaagggagtaattgg 426 272 TCAAAAGGCAGAAATTGAAAGTCAAAAGGCAGAAATTGAAAGTCAAAAAGGCAGAAATTGA 213 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segrefigenoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to 8 kb were prepared and both extremities were sequenced. See Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000) Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, F., Epingsare, Olarente, B., de-Montigny, J., Dujon, B., Durrens, P., Lepingsare, Llorente, B., de-Montigny, J., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Janes, A., Calon, J., Changa, J., Calon, CNS07CVP 1005 bp DNA linear GSS 08-JUL-2001 T3 end of clone BD0AA007C03 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence. Similarity 57; Conserv Genoscope.
Direct Submission Candida tropicalis FEBS Lett. 487 (1), 91-94 (2000) 20584726 Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. Candida tropicalis. AL439691.1 GI:12223104 AL439691 Genomic exploration of the hemiascomycetous yeasts: 16. Candida Dujon, B. keywords for description of this sequence and for the sequence of tropicalis (bases 1 to 1005) (bases 1 to 1005) (bases 1 to 1005) 146 Conservative Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)." Ø 2.0%; 193 0; Score 43.2; DB 12; Pred. No. 0.59; Mismatches 23; Length 844; 0 Gaps 0

VERSION KEYWORDS

TITLE

COMMENT

TITLE

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                                                                                              Tel: +55-11-2704922
Feax: +55-11-2707001
Email: astmpson@ludwig.org.br
Email: astmpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMI&t2=PMI-NN1200-
271100-008-f12&t3=2000-11-27&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 163.
Location/Qualifiers
Location/Qualifiers
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1 (bases 1 to 228)

Dias Neto, E.; Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Badai, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Query Match Best Local Matches ch 2.0%; l Similarity 71.8%; 56; Conservative 0; Pred. No. 0.35; Mismatches Indels Length 228; 0;

ORIGIN BASE COUNT

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В Qy 148 249 ccctcttgtcccgcctgt 266 CGGGGCTGTCGGGCTAGT 165

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Search completed: August 20, 2002, 15:39:26 Job time: 9549 sec

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SUMMARIES

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1 (bases 1 to 518)
Morsey,M.A. and Sheppard,M.G.
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1 (bases 1 to 5108)

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Morsey, M.A. and Sheppard, M.G.

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artificial sequence.

1 (bases 1 to 5108)

Morsey,M.A. and George,M.

Growth hormone and growth hormone-releasing ho
patent: JP 200035590-A 50 19-DEC-2000;

PPTZER PROD INC
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PN JP 2000350590-A/50
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PF 12-APR-2000 JP 2000111120
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Growth hormone and growth
BD000697
BD000697.1 GI:18623810
JP 2000350590-A/50.
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CE 1 (bases 1 to 5108)

RS Morsey, M. A. and George, M.

AL Patent: JP 2000350590-A 51 19-DEC-2000;

PATER PROD INC

OS Artificial Sequence
PN JP 2000350590-A/51

PD 19-DEC-2000
PF 12-APR-2000 JP 2000111120
PF 12-APR-2000 JP 2000111120
PR 12-APR-1999 US 60/128830
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JP 2000350590-A/51.
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Sequence 55
AX138936
                                                                                                                                                                                                                  artificial sequence.
1 (bases 1 to 5111)
Morsey,M.A. and Sheppard,M.G.
Growth hormone and growth hormone releasing hormone compositions patent: EP 1052286-A 55 15-NOV-2000;
Pfizer Products Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                        synthetic construct
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, 1314 c 1230 g 1287 t
                                                                                                                                                                                                                                                                                                               5111 bp
from Patent EP1052286.
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94.5%;
                                                                                                                             ; Score 2149.4;
; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                         DNA
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                                                                                                           artificial sequence.

1 (bases 1 to 5111)
Morsey, M.A. and George, M.
Growth hormone and growth ho
Patent: JP 2000350590-A 54 1
PFIZER PROD INC
OS Artificial Sequence
PN JP 2000350590-A/54
PD 19-DEC-2000 JP 20001111
PF 12-APR-2000 JP 20001111
PF 12-APR-1999 US 60/12
PI MOHAMBED ALI MORSEY, MIC
PC C12N15/09, A01K67/027, A6
PC A61P5/02,
PC A61R37/36, C07K14/60, C12
PC A61K37/36, C12N5/00, (C12
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PC A61K37/43, C12N5/00, C12
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JP 2000350590-A/54.
synthetic construct.
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Similarity 94.5%;
93; Conservative
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JP 2000350590-A/54
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12-APR-1999 US 60/128830
MOHAMMED ALI MORSEY, MICHAEL GEORGE
C12N15/09, A01K67/027, A61K31/711, A61K38/27, A61K38/04, A61K48/00,
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Location/Qualifiers
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.57	TGACTCGGGGGGGGGGGG 1	4441 1514	DP QA
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440	4	4441	Qy
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7	ggaaaaagagttggtagctcttgatccggcaaaccaaccgctggtagcggtggtttt 42 	4226 1214	рь
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)93 .	gtottgagtocaacccggtaagacacgacttatcgccactggcagcagccactggtaac 41 	4046 c	Qу
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RESULT 8
AX138928
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX138928 5185 bp Sequence 47 from Patent EP1052286. AX138928 AX138928.1 GI:14274633

DNA

linear PAT 30-MAY-2001

synthetic construct.

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77	cggatacatatttgaatgtatttagaaaaataaacaaataggggttcc	Qy
TCTCATGA 28	CGTGGCTTTCCCCCCCCCCCCATTATTGAAGCATTTATCA	Db
gtctcatga 571	5653 caacgtggctttccccccccccccattattgaagcatttatcagggttattg	Qy
TTTTGAGACA 277	ATGATGATATTTTTATCTTGTGCAATGTAACATCAGAGA	Db
ttttgagaca 56	tattgttcatgatgatatatttttatcttgtgcaatgtaacatcagaga	Qy
GCAGACAGTT 271	GAATATGGCTCATAACACCCCTTGTATTACTGTTATGTAA	Db
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AGCAAGAC	TAAATCAGCATCCATGTTGGAATTTAATCGCGGCCT	Db
agcaagacg 553	tttatacc	Qy
TCGCGAGCC	CGATAGATTGTCGCACCTGATTGCCCGACATTA	Db
tcgcgagccc 547	gggcttcccatacaatcgatagattgtcgcacctgattgcccgacatta	Qу
CIGGCGCAT 25	TGGCAACGCTACCTTTGCCATGTTTCAGAAACAACT	Db
ctggcgcat 541	atctgtaacatcattggcaacgctacctttgccatgtttcagaaaccaact	Qy
TGACCATCT 24	CGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTC	Db
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AGTACGGA 241	TTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCA	Дb
29	gaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatca	Qy
CTAATACCT 2	GCCAGCGCATCAACATATTTTCACCTGAATCAGGATATTCTT	Дδ
ctaatacct 523	gaacactgccagcgcatcaacaatattttcacctgaatcaggatattctt	Qγ
CGGCGCA 22	TANAAGGACAATTACAAACAGGAATCGAATGC	da.
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1 (bases 1 to 5185)

2 1 (bases 1 to 5185)

3 Morsey, M.A. and George, M.

5 Morsey, M.A. and George, M.

6 Morsey, M.A. and George, M.

7 Patent: JP 2000355590-A 46 19-DEC-2000;

8 PR 12-APR-2000

8 PR 19-DEC-2000

9 PR 12-APR-2000 JP 2000111120

9 PR 12-APR-1999 US 60/128830

9 PR 12-APR-1999 US 60/128830

9 PR 12-APR-2000 JP 2000111120

9 PC MOHAMMED ALI MORSEY, MICHAEL GEORGE

9 PC A6115/02,

9 PC A6115/02,

9 PC A611837/36, C12N5/10/(C12N5/10,C)

9 PC A61837/36, C12N5/00, C12N5/00,C12R1:91)

9 PC A61837/36, C12N5/00, C12N5/00,C12R1:91)

9 PC A61837/43,C12N5/00,C12N5/00,C12R1:91)

9 PC A61837/43,C12N5/00,C12N5/00,C12R1:91)
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A61K37/43,C12N5/00,(C12N5/00,C12R1:91)
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1 (bases 1 to 5188)
Morsey,M.A. and Sheppard,M.G.
Growth hormone and growth hormone rele
Patent: EP 1052286-A 59 15-NOV-2000;
Pfizer Products Inc. (US)
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1 (bases 1 to 5188)
MOTSBEY, M.A. and George, M.
Growth hormone and growth ho
Patent: JP 2000350590-A 58 1
PFIZER PROD INC
OS Artificial Sequence
PN JP 2000350590-A/58
PD 19-DEC-2000 JP 20001111
PF 12-APR-2000 JP 20001111
PF 12-APR-1999 US 60/12
PI MOHAMMED ALI MORSEY, MIC
PC C12M15/09, A01K67/027, A6
PC A61P5/02,
PC A61R37/36, C07K14/60, C12
PC A61K37/36, C12N5/00, (C12
PC A61K37/36, C12N5/00, (C12
PC A61K37/43, C12N5/00, C12
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12-APR-1999 US 60/128830
MOHAMMED ALI MORSEY, MICHAEL GEORGE
C12N15/09, A01K67/027, A61K31/711, A61K38/27, A61K38/04, A61K48/00,
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4872	agccgtttctgtaatgaaggagaaaactcaccgaggcagttccataggatggcaagat	8	Оу
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1873	AATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATTAGAAAAAACTCAT	1814	Ф
4752	agcgtaatgctctgccagtgttacaaccaattaaccaattctgattagaaaaaactcat	4693	Qy
1813	CTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGCCGTCCCGTCAAG	1754	DЬ
4692	tctgatccttcaactcagcaaaagttcgatttattcaacaaagccgccgtcccgtcaag		Qy
1753	TIGGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTG	1694	Db
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4452	666666666666	4441	Qy
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4440		4	Qy
1453	AAAT	39	Db
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1033	CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCCTTATCCGGTAACTAT	974	Db

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AL Patent: JP 2000350590-A 59 19-DEC-2000;

PRIZER PROD INC
OS ATTIFICIAL Sequence
PN JP 2000350590-A/59
PD 19-DEC-2000
PF 12-APR-2000 JP 2000111120
PF 12-APR-1999 US 60/128830
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Morsey,M.A. and George,M.
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	ry Match 36.7%; Score 2149.	⊆

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Kendall, R.L., Thomas, K.A., Bett, A.J. and Huck Kendall, R.L., Thomas, K.A., Bett, A.J. and Huck Gene therapy for stimulation of angiogenesis game therapy for stimulation of angiogenesis gene therapy for stimulation of angiogenesis generally 50 patents. We gold the stimulation of the state 
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4177 AGGAACATGCCAGCGCATCAACAATATTTCACCTGAATCAGGATATTCTTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg [5712	Qy
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4177 AGGAACCTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCAATACC 5232 tygaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg		N	65	Qy
4177 AGGAACATGCCAGCGCATCAACAATATTTCACCTGAATCAGGATATTCTTCATATACC 5232 tggaatgctgttttcccggggatcgcagtggtggtgagtaaccatgcatcatcaggagtacgg			4597	Db
4177 AGGAACATGCCAGCGCATCAACAATATTTCAGCTGAATCAGGATATTCTTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg			5592	Qу
4177 AGGAACACTGCCAGCGCATCAACAATATTTCACCTGAATCAGGATATTCTTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg			4537	рЪ
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4177 AGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg			4357	Db
4177 AGGAACATGCCAGCGCATCAACAATATTTTCAGCTGAATCAGGATATTCTTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg		2	5352	Qy
4177 AGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg [4297	Вр
4177 AGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg		N	5292	Qy
4177 AGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTCTAATACC 5232 tggaatgctgttttcccggggatcgcagtggtgagtaaccatgcatcatcaggagtacgg			4237	DЬ
4177 AGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACC			5232	Qy
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              DNA sequence of sh Human leukocyte al Vaccine vector VlJ Vaccine vector VlJ VlJns-tPA vector t VlJns-tPA vector t Plasmid GHRH1-29YW
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vR-1012 D	40	21	4912	36.6	214
ρVR	939	20	7272	5	143.
DNA of pVR 1012-GP	AAX89796	20	7073	6.	143.
ression v	AAQ74207	15	4864	6.	143.
Bicistronic chimer	AAF30315	22	7521	6.	145.
pVR 1	AAX89798	20	7272	6	145.
1 pvR 1012-	AAX59391	20	7073	6.	145.
e of a	AAH22810	22	8366	6.	146.
Bicistronic idioty	AAF30316	22	7528	6.	146.
smid pvR 1012-	AAX59392	20	7285	σ.	2146.8
DNA of pVR 1012-GP	AAX89797	20	7285	σ.	146.
DNA sequence of a	AAH22814	22	7099	5	146.
Bicistronic idioty	AAF30341	22	6729	σ.	146.
Bicistronic plasmi	AAF30339	22	6709	σ,	146.
Cytokine-encoding	AAX81562	20	5480	٥.	146.
Cytokine-encoding	AAX81677	20	5469	٥.	146.
Cytokine-encoding	AAX81560	20	5428	6.	146.
Cytokine-encoding	AAX81564	20	5422	σ.	146.
Mouse Flt-3 ligand	AAF30313	22	5322	6.	146.
Plasmid VR4151, co	AAA63225	21	5322	σ,	146.
ne-enc	AAX81563	20	5322	6.	146.
Human Flt-3 ligand	AAF30314	22	5310	6.	146.
Cytokine-encoding	AAX81565	20	5259	σ.	146.
Cytokine-encoding	AAX81561	20	5259	6.	
Vaccine vector V1R	AAD09623	22	4864	6	146.
	AAD09613	22	4864	6.	146.
Vector	AAD09437	22	4864	٥.	146.
e vector	94	22	4864	6.	146.
VEGF (145)	AAX57727	20	4864	6.	146.
neo seq	AAV21737	19	4864	6	146.
ression vector	AAT01114	16	4864	σ.	146.
DNA sequence for e	AAS09198	22	4862	٥.	146.
-	303	22	4779	σ.	146.
lasmid	8626	22	5254	6	9
d GHRH1-44Y	862	22	5188	6	149.
pGHRH-4 construct.	AAC86254	22	5185	36.7	

ALIGNMENTS

RESULT AAS18308 Cloning vector; Ketogulonigenium replicon; endogenous plasmid; mutant transformed host cell; Escherichia coli; pADM291-4; circular; cyclic; shuttle vector plasmid; ds. Ketogulonigenium sp. strain ADM291-19 Synthetic. AAS18308 standard; DNA; 5859 D'Elia J; 05-APR-2000; 2000US-194625P 18-OCT-2001 WO200177347-A2 DNA sequence of shuttle vector plasmid pADM291-4. 12-MAR-2002 (first entry) 05-APR-2001; 2001WO-US11059 (ARCH) ARCHER-DANIELS MIDLAND CO ВP

promoter

WPI; 2002-049150/06

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Query Match
Best Local Similarity
Matches 5859; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, pADM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coli, enable the cloning of certain genes of Ketogulonigenium in E.coli as the latter is an efficient host for amplification of vector DNA. The present DNA sequence represents the shuttle vector plasmid pADM291-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid vector comprising Ketogulonigenium replicon found a specific deposited endogenous plasmid, useful for producing polypeptides and/or transcripts by culturing host cells transformed with vector .
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XX AAH79219;
AC AAH79219;
XY 20-NOV-200
XX Human leuk
XX Human; leu
XX Unidentifi
XX RU21654555
XX 20-APR-200
XX 23-NOV-199
                                    RU2165455-C1
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                                                                                        leukocyte
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                                                                                         alpha-2b interferon
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Shevchuk AA, Fedyukin VS, r
Sventitskii EN, Urakov NN,
Martyushin SV, Ishchenko AM,
Shalaeva ON, Lisitskaya VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to cells of recipient strain Escherichia coli BL 21 (DE3), which are transformed by recombinant multicopy plasmid DNA pSS5 encoding leukocyte human alpha-2b interferon. Expression of the latter is under control of a lactose gene, phage T7 and tryptophan promoters and the terminator of translation rrn B-T1T2, containing a gene determining resistance to kanamycin and containing a DNA fragment from plasmid pUC19 that is responsible for replication of recombinant plasmid. The cells can be used in biotechnology, molecular biology and genetic engineering. The invention can be used for preparing recombinant human leukocyte alpha-2b interferon for medicinal use. The present requesce is an oligonucleotide described in the exemplification of the
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Nikolaev TM, Tolkachev BB;
Kalinin YU T, Denisov LA, Ty
M, Trofimov AV, Polyakova EA,
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The present invention relates to a pharmaceutical DNA vaccine compositic comprising an expression vector and a DNA molecule containing a codon optimised open reading frame encoding HIV-1 Pol protein or its inactivated form. HIV-1 Pol protein or its inactivated form the protein or its inactivated form generates a cellular immune response against human immunodeficiency virus-1 (HIV-1) infection. The DNA vaccine is useful for inducing an immune response against infections or diseases caused by virulent strains of HIV in a payalist infection of diseases caused by virulent strains of HIV in a human. The protein encoded by the DNA vaccine is useful as a protein-based HIV vaccine. The present sequence is a vaccine vector VIJ based in the preparation of DNA vaccine. VIJ comprises human cytomegalovirus (CMV)intA promoter, bovine growth hormone (BGH) transcription termination elements, SfiI restriction sites adm kanamycin and ampicillin resistance genes.
                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide vaccine composition for immunization against human immunodeficiency virus infection or to combat existing HIV conditions DNA molecule containing codon optimized HIV-1 Pol or modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shiver JW,
                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 42-45;
Sequence
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  4867
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  1231 A; 1226 C; 1173 G; 1237 T; 0 other;
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                    WO200143693-A2
                                                           human
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                                                                vaccine; c
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                                                           immunodeficiency
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                                Human cytomec
Bos sp.
Unidentified
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                                                                immune
                                             cytomegalovirus
                                                                optimisation; Nef protein; HIV infection; ne response; cytotoxic T lymphocyte; CTL;
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                                                                                                  entry)
                                                           response;
cy virus;
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                                                           HIV;
                                                           lymphocyte; vector; ds.
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Example 1; Page 33-35; 84pp; English.
                                                                                                                                                     Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                   Shiver JW, Liang X,
                                                                                                                                                                                                                   (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                               15-DEC-2000;
                                                                                                                                                                                       2001-417878/44.
                                                                                                                                                                                                                                             2000WO-US34162
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The present invention relates to a DNA vaccine comprising a DNA CC expression vector, and a DNA molecule containing a codon optimised open CC reading frame encoding a wef protein or its immunogenic derivative. The CC Nef protein or its derivative is expressed and generates an immune CC infection, upon administration of to a host. The DNA vaccine is useful CC response which provides a substantial level of protection against HIV CC for inducing a cell mediated immune (cytotoxic Tlymphocyte, CTL) CC by administering the DNA vaccine into the tissue of the vertebrate host, CC preferably human. It is also useful for lowering transmission rate to CC preferably human. It is also useful for lowering transmission rate to CC codes within an infected individuals and/or for reducing levels of viral CC phase of HIV infection. The present sequence is a vaccine vector cCC vlns with Sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with Sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with Sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus intron A promoter, CCC vlns with sfil site comprises human cytomegalovirus

Sequence 4867 BP; 1231 A; 1226 C; 1173 G; 1237 T; 0 other:

DB 22; Length 4867;

δÃ 밁 Qy ДЬ Qγ 망 δÃ 밁 Qy В δÃ DЬ Qγ DЪ δÃ Query Match
Best Local Similarity
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3881 cctggtatcggtctgcgattccgactcgtccaacatcaatacaacctattaatttcccct 394	Db
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Best Local Similarity 94.5%;
Matches 2293; Conservative
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                                                                                                                                                                                                                                       The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open creading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral loads within an infected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is a vaccine vector VlJns-tPA to construct human tissue-specific plasminogen activator (tPA) and HIV-1 pol DNA fusion construct.
                                                                                                                                           Query Match
Best Local S
Matches 2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, at DNA containing codon optimized open reading frame encoding Nef prot
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                                                                                                                                                          Local Similarity
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mediated immune response; cytotoxic T lymphocyte; CTL;
n immunodeficiency virus-1; HIV-1; VlJns-tPA vector; ds.
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                                                                                                       Query Match 36.7%;
Best Local Similarity 94.5%;
Matches 2293; Conservative
                                                                                                                                                                                                                                                                             The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve growth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional chemical methods. They have enhanced resistance to enzymatic degradation, therefore have increased length of activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examples; Page
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enhanced resistance to enzymatic degradation, useful for treating
growth hormone deficiency related disorders or to improve growth
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                                          which contains the cytomegalovirus immediate-early gene promoter, cenhancer, and 5' untranslated sequences followed by a multiple cloning site for inserting genes to be expressed. The transcriptional terminator region includes the polyA and termination signals from the rabbit beta-globin gene. VR1051 is used as a DNA mass control for VR6200 (see AAF30313), which expresses a secreted form (see AAB20187) of mouse Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to chancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo a Flt-3 ligand-encoding polynucleotide such as VR6200, and 1 or more antigen- or cytokine-encoding polynucleotides.
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ttttat cccatt cccatt	gatty atcca atcca 		caaacc caaacc aggaca aggaca aatatt	actcg actcg agagaa ttcca	tacaac tacaac ttatto !ttatto gaaaac
cttgt	cctts	ggtga ggtga ggtga aaatt aaatt	gttatt gttatt attaca ttcacc	ccaac ccaac tcacc tcacc	caatt
caatg caatg caatg gcatt aacaa	ctgatt ctgatt ctgattta aattta tattac	taacc taacc cgtca cgtca	cattcg aacagg aacagg	tcaat tcaat tgagt tgagt	accaat ggatt aggca
aacat atcag taggg	gcccga gcccga atcgcg atcgcc 	tgcat	tgatto aatcg aatcg aatcg	acaacc gacgac gacgac	tctgat tctgat tcaat; ttcaa ttcca
agaga gttat ttat ttccg	cattat - - - -	catcagg	cgcct	taa taa atc atc	tagaaa ccata ccata ccata aggat
tttttga ttttga ttttga tgtctc tgcaca gcgcaca	cgcgag agcaag cagaca	gagtac tgacca tgacca	agcgan agcgan ccggc ccggc	tttccc cggtga cggtga acgctc	aactc: :tttg :ttttg :ltttg :jgcaag
gac 56! gac 43 atg 57 atg 43 attt 57	Jcc 547 1 3 3 3 1 1 4 4 5 5 1 1 4 4 6 7 7 8 8 9 1 1 1 1 1 1 1 1 1 1	gg 529 gg 396 tc 535 tc 402 tc 402	ga 5111 	9 499 9 366 9 372	1 475 1 347 1 348 1 348 1 348 1 348 1 348
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                                                                                                                                                                                                                                                CC The present invention relates to a method for determining the amount CC of fusion that occurs between two cells, one of which contains the CC enzyme beta-lactamase and the other of which contains a fluorescent CC substrate of beta-lactamase. The method comprises the measurement of CC fluorescence resonance energy transfer (FRCT). The invention also CC provides methods of identifying inhibitors of the fusion of two CC types of cells, particularly when fusion is mediated by the CC interaction of a viral protein and target cellular proteins e.g. CD4 CC and cytokine receptors. The methods are useful for identifying CC substances that are useful for the treatment of viral diseases, CC particularly for the identification of inhibitors of HIV-1 infection. The present DNA sequence for expression vector pVlJneo is used in the CC methods of the present invention.
                                                                                                                                       Query Match
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inhibition of cell fusion; CD4; cytokine re
inhibition of cell fusion; CD4; cytokine re
inhibition; pVlJneo; cyclic; circular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide vaccine; genetic immunization; coordinate expression; HIV-1; AIDS; human immunodeficiency virus; antigen; immunogen; CMVintA-GBH; vector; plasmid VlJneo; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT01114 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression vector
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                                                                                                                                                                                 Vector VlJneo (AAT01114) was obtd. from vector VlJ (AAT01113) by replacement of the ampicillin-resistance gene with a neomycin-resistance gene. The vector also contains a CMVintA-GBH terminator construct (AAT01112) providing controlled expression of heterologous genes. Insertion of HIV antigen genes into the vector allows large-scale production of polynucleotide vaccine in bacterial host
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1tttcccc 4931 1tttcccc 3936	2 tootggtatoggtotgogattocgactogtocaacatcaatacaacotattaa 	487 387	Оу	
:ggcaaga 4871 :ggcaaga 3876	2 aaaagccgtttctgtaatgaaggagaaaactcaccgaggcagttccataggat 	481 381	Qу	
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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US-08-663-998-2
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US-08-316-950-15
PCT-US95-12642-15
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CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,998
FILING DATE: 06-JUN-1996
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: KOWALSKI THOMBER: 32,147
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5900 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLETIF TYPE: DNA (genomic)
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                     Query Match
Best Local Similarity
Matches 2292; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HUEBNER, Robert C.
APPLICANT: NORMAN, Jon A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: ADMINISTERING BORRELIA DNA
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-08-811-877-3
US-09-058-746-1
US-09-438-142-1
US-09-23-134-1
US-09-23-535-1
US-09-23-535-1
US-07-977-630-1
US-07-977-630-2
US-07-978-630-2
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US-07-978-630-2
US-07-977-630-2
US-07-977-630-2
US-07-977-630-2
US-07-977-630-2
US-08-246-403A-4
                     Score 2146.8;
Pred. No. 0;
0; Mismatches
                       0;
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Score

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В ? 2

Indels 134; Length 5900;

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Minimum DB Maximum DB

Scoring table:

Title: Perfect score:

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Ca 45/1	4512 atcatccagccagaaagtgagggagccacggttgatgagagctttgttgtaggtggac	Qy
	CCTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCCTGAATCGCC	дь
2 60	4452 gcgctgaggtctgcctcgtgaagaaggtgttgctgactcataccaggcctgaatcgcc	Qу
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- 444	gattatcaaaaaggatcttcacctagatcctttt	Ωу
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c 4165	106 aggattagcagagcgaggtatgtaggcggtgctacagagttcttgaagtggtggcctaa	Qy
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APPLICANT: HUEBNER, Robert C.
APPLICANT: LIANG, Xiaowu
APPLICANT: LIANG, Xiaowu
APPLICANT: CANNER, KIStin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine JO.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: ADMINISTERING BORRELIA DN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/663,998
FILLING DATE: 06-JUN-1996
CLASSIFICATION NUMBER: US/08/663,998
FILLING DATE: 06-JUN-1996
CLASSIFICATION NUMBER: 32,117
REGISTRATION NUMBER: 33,117
REGISTRATION NUMBER: 454312-2440
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5952 base pairs
TYPE: nucleic acid
TYPE: DUCLEIC acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-663-998-2
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Best Local Similarity 94.4%;
Matches 2292; Conservative
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                                                               Score 2146.8;
Pred. No. 0;
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                         ATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGGAGCTTTGTTAGGTGGACCA
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                                                     Query Match
Best Local Similarity
Matches 2291; Conser
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,998
FILING DATE: 06-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REGISTRATION NUMBER: 32,147
                                                                                                                                                                                                              TELEPHONE: 212-840-3333 INFORMATION FOR SEQ ID NO:
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APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristlin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
APPLICANT: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: ADMINISTERING BORRELIA DNA
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LENGTH: 5676 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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TOPOLOGY: lin
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Patent No. 584694
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Best Local Similarity
Matches 2291; Conserv
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NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STREET: 530 Fif
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
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-663-998-4
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                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Application US/08663998
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Pred. No. 0;
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                               AGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTT
                                                                     ACAACGTGGCTTTCCCCCCCCCCCCCATTATTGAAGCATTTATCAGGGTTATTGTCTCATG
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US-08-316-950-15/c

; Sequence 15, Application

; Patent No. 5679515
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, NAME/KBY: misc_feature

; LOCATION: 1.4296

OTHER INFORMATION: /sti

US-08-316-950-15
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4296 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Applicat Patent No. 5679515
GENERAL INFORMATION:
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 2011; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,950
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5411
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend
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1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Steuart Street Tower, CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                 agcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttccataggctccgcc
                                                                                                                                                              CCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAA
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RESULT 6
PCT-US95-12642-15/c
Sequence 15, Application PC/TUS9512642
; Sequence 15, Application PC/TUS9512642
; GENERAL INFORMATION:
APPLICANT: PathoGenesis Corporation
APPLICANT: 201 Elliott Avenue West, Suite 150
APPLICANT: Seattle, Washington 98119
TITLE OF INVENTION: Mycobacterial Reporter Strains and TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Stewart Street Tower, One Market Plaza
COUNTRY: US
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 2011; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS
SOFTWARE: PATENTIN Releac
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCTJ
FILING DATE: 02-OCT-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..4296
OTHER INFORMATION: /standard_name= "plasmid-
-US95-12642-15
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FEATURE:
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APPLICATION NUMBER: US 08/316,
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
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02-OCT-1995
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                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, \
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/316,950
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNCET, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15371A-0
TELECOMMUNICATION: 10FORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9601
TELEPHONE: (415) 543-9610
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                                     MOLECULE TYPE: FEATURE:
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CITY: Sa
STATE: C
COUNTRY:
                                                               LENGTH: 4352 base partype: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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NAME/KEY: misc_feature LOCATION: 1..4352 OTHER INFORMATION: /sta
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                                                          ccccttgtattactgtttatgtaagcagacagttttattgttcatgatgatatattttta
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; LOCATION: 1..4352
; OTHER INFORMATION: /standard_name=
PCT-US95-12642-16
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PCT-US95-12642-16/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application PC/TUS9512642 GENERAL INFORMATION:
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Best Local Similarity
Matches 2011; Conser
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12642
FILING DATE: 02-OCT-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Steuart Street Tow
CITY: San Francisco
STATE: California
COUNTRY: US
2IP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Computible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
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APPLICANT: 201 Elliott Avenue West, Suite 1
APPLICANT: Seattle, Washington 98119
TITLE OF INVENTION: Mycobacterial Reporter
TITLE OF INVENTION: Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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APPLICANT: STOVER, Charles APPLICANT: HICKEY, Mark J. TITLE OF INVENTION: Mycobac TITLE OF INVENTION: Thereof

Mycobacterial Thereof

Reporter

Strains

and Uses

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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

d Townsend Khourie Tower, One Market

and Crew

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0

#1.0,

Version

#1.25

ADDRESSEE: Townsend and To STREET: Steuart Street To CITY: San Francisco STATE: California COUNTRY: US 2IP: 94105-1493

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              RESULT 9
US-08-316-950-12/c
    sequence 12, Application
patent No. 5679515
Patent No. 5679515
GENERAL INFORMATION:
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US-08-316-950-12
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TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9603
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6047 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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APPLICATION NUMBER: US/08/316,950
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15371A-001100
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION:
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                      gaaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaaagagttg
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, OTHER INFORMATION: /sts
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICANT: 201 Elliott Avenuest, Suite 150
APPLICANT: Seattle, Washington 98119
TITLE OF INVENTION: Mycobacterial Reporter St
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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FILING DATE: 02-OCT-
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                               REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15371A-001100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                APPLICATION NUMBER: US 08/316,950 FILING DATE: 03-OCT-1994 ATTORNEY/AGENT INFORMATION: NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie
STREET: Steuart Street Tower, One Market
CITY: San Francisco
STATE: California
COUNTR: US
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                                                             MOLECULE TYPE:
                                                                                                                                                                                                      NAME: Hunter, Tom
REGISTRATION NUMBER:
                                                                           TOPOLOGY:
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TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,950
FILING DATE: 03-CCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER; Tom
REGISTRATION NUMBER: 15371A-0011
REFERENCE/DOCKET NUMBER: 15371A-0011
TELEPOMMUNICATION INFORMATION:
TELEPANE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENUTH: 303 base Dates
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Best Local Similarity
Matches 2000; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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APPLICANT: HICKEY, Mark J.
TITLE OF INVENTION: Mycobacterial Reporter
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 18
                  3873
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CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                             caggactataaagataccaggcgtttccccctggaagctccctcgtgcgctctcctgttc
                                                                                                         TCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGA
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Pred. No. 0;
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APPLICATION DATA

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    Sequence 14, Application PC/TUS9512642
    GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1264
FILING DATE: 02-OCT-1995
CLASSIFICATION:
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APPLICANT: 201 Elliott Avenue West, Suite 1
APPLICANT: Seattle, Washington 98119
TITLE OF INVENTION: Mycobacterial Reporter
TITLE OF INVENTION: Thereof
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                                                                                                          COUNTRY: ZIP: 941
                                                                                                                                ADDRESSEE: Townsend
STREET: Steuart Stre
CITY: San Francisco
STATE: California
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..3993
OTHER INFORMATION: /standard_name=
PCT-US95-12642-14
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FILING DATE: 03-OCT-1994
ATTORNET AREAT INFORMATION:
NAME: HUNLET, TOM
REGISTRATION NUMBER: 38,498
REFERENCE_DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9640
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
IENUTERISTICS:

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Local Similarity 95..
2000: Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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               agaggcataaattccgtcagccagtttagtctgaccatctcatctgtaacatcattggca
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LOCATION: 1..6044
; LOCATION: 1..6044
; OTHER INFORMATION: /stand
; OTHER INFORMATION: pMV361-
US-08-316-950-18
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                                                                                                                                                                                                         NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE, DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08316950 Patent No. 5679515
Query Match
Best Local Similarity 95.0
Matches 2000; Conservative
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APPLICANT: STOVER,
APPLICANT: HICKEY,
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08,
FILING DATE: 03-0CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mycobacterial Reporter Strains (
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                           ataacaccccttgtattactgtttatgtaagcagaccagttttattgttcatgatgatata
                                                                           gcatccatgttggaatttaatcgcggcctcgagcaagacgtttcccgttgaatatggctc
                                                                                                              tagattgtcgcacctgattgcccgacattatcgcgagcccatttataccccatataaatca
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                                                                    GCATCCATGTTGGAATTTAATCGCGGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTC
                                                                                                      TAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCCATTTATACCCCATATAAATCA
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                                 ATAACACCCCTTGTATTACTGTTATGTAAGCAGACAGTTTTATTGTTCATGATGATATA
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RESULT 14
PCT-US95-12642-18/c
; Sequence 18, Application
; GENERAL INFORMATION:

PC/TUS9512642

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OTHER INFORMATION: ;
OTHER INFORMATION: ;
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FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6044 base pairs
TYPE: nucleic acid
STEAMDERNESS: $10716
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 2000; Conserv
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PathoGenesis Corporation
APPLICANT: 201 Elliott Avenue West, Suite 1
APPLICANT: Seattle, Washington 98119
TITLE OF INVENTION: Mycobacterial Reporter
TITLE OF INVENTION: Thereof
                 3873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..6044
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                                         CAGGACTATAAAGATACCAGGCGTTTCCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTC
                                                                                            tccgccccctgacgagcatcacaaaaatcgacgctcaagtcagaggtggcgaaacccga
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95.6%;
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pMV361-lux"
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      agtgagaaatcaccatgagtgacgactgaatccggtgagaatggcaaaagcttatgcatt 5012
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AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAA
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US-07-977-630-20/c
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Patent No. 5583038
                                                    STREET: 6 Becker farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READNALE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                  APPLICANT: Stover, Char
TITLE OF INVENTION: BAC
TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
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    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,
FILING DATE: NO. 5583038ember
CLASSIFICATION: 435
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                               COMPUTER: IBM
OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                              ADDRESSEE: Stewart & C
STREET: 6 Becker Farm
                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                     Carella, Byrne, Bain,
Stewart & Olstein
INFORMATION
                                                                                                                          Charles K.
BACTERIAL EXPRESSION VECTORS CONTAINING
DNA ENCODING SECRETION SIGNALS OF LIPOPP
: 84
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              1993
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4120 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: nucleic acid
S-07-977-630-20
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Best Local Similarity
Matches 1996; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cacgctgtaggtatctcagttcggtgtaggtcgttcgctccaagctgggctgtgtgcacg
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                ggacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaaagagttggta 4241
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acgctcagtggaacgaaaactcacgttaagggattttggtcatgagattatcaaaaagga
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0; Mismatches
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19301.790 Million cell updates/sec
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AL640799 AL640799
AL660035 AL640799
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AL637190 AL637190
AL654693 AL654693
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AJ281480 4A3A-P4G8
AL645114 AL645114
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ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT AJ281449 LOCUS SOURCE FEATURES COMMENT REFERENCE DEFINITION MEDLINE TITLE AUTHORS ORGANISM JOURNAL source Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. Anopheles gambiae pilot gene discovery project: identification mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) ; Anopheles.
1 (bases 1 to 800)
1 (bases 1 to 800)
Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B. Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea Anopheles gambiae Eukaryota; Metazoa 4A3A-P4D5-F Anopheles gambiae immune compete gambiae cDNA clone 4A3A-P4D5, mRNA sequence. Contact: Dimopoulos G and Kafatos, F.C African malaria mosquito AJ281449.1 GI:6929329 20300950 /organism="Anopheles gambiae"
/strain="4A r/r"
/db_xref="4A x/r"
/db_xref="4A3A-p4D5"
/clone="14A3A-p4D5"
/clone="14A3A-p4D5"
/cell_line="immune competent 4A3A"
/cell_line="immune competent 4A3A"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line Location/Qualifiers dq 008 p mRNA linear EST 30-JUN-2000 immune competent 4A3A Anopheles

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9ambiae cDNA
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African mala)
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                                      CDNA
 malaria
                                     Anopheles gambiae
A clone 4A3A-P4G8,
                   GI:6929360
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 GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae pilot gene discovery project: mosquito innate immunity genes from expressed so generated from immune-competent cell lines proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6620
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Fotis C. Kafatos laboratory
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Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,I
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Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="4A3A-P4G8"
/clone=11b="Anopheles gambiae immune competent /cell_line='immune competent 4A3A"
/lab_host="E. coli_DH10B"
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/strain="4A r/r"
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aaaggcggtaatacggttatccacagaatcaggggataacgcaggaaagaacatgtgagc 3690
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Huckle, E., Taylor, R., Ashurst,
Sanger Xenopus tropicalis EST
Unpublished (2001)
Contact: Huckle E
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This sequence is from a Xenopus constructed by Aaron M. Zorn.
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Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project:
TROPICALIS_SEQUENCE_ID: TNeu017b19.sp6
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                                                                                                                                                                                                                                                                                                    /dev_Stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
/note="Vector: pCS107; Site_2: NotI; cDNA
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/clone_lib="XGC-neurula"
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AL419357
AL419357.1 GI:12202535
2 (bases 1 to 988)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolottin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                             de Montigny, J., Spehner, C., Wincker, P., Artiguenave, F., Genomic exploration of the
                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; 1 (bases 1 to 988)
                                                                                                                                                                              Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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                                                                                     FEBS Lett.
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiyuus, Saccharomyces servazzii, Zygosaccharomyces rouxii, exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Incention/Qualifiers
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                                                                                                     Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts:
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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DKFZP434C172_s1 434 (synonym:

DKFZP434C172 3', mRNA sequence

AL044364 GI:5432586
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This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; 1 (bases 1 to 954)
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This clone (DKFZp434C172) is available at the RZPD in B Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
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nilarity 99.9%;
Conservative
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Pred. No. 4e-163;
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/tissue_type="Kidney
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Kono, T., Sakal, M. and Lapatra, S.E.
Expressed Sequence Tag Analysis of Kidney and Gill T Rainbow Trout (Oncorhynchus mykiss) Infected with In Hematopoletic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai
                                                                                                                                                                                                                                                                                                                            AU081137 1067 bp mRNA linear EST 30-AUG-7 AU081137 Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KI2,
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EST.
                                                                                                            Faculty of Agriculture Miyazaki University
                                                                                                                                                                                                                                                                        rainbow trout.
                                                                        nishi gakuenkibanadai, Miyazaki,
il: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
/organism="Oncorhynchus my
/db_xref="taxon:8022"
/clone="K12"
/clone_lib="Oncorhynchus m
infectious hematopoietic n
                                                 mykiss'
 mykiss Kidney
necrosis virus
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  virus"
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            infected
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4 4A3A-P6F11-F Anopheles gam
gambiae cDNA clone 4A3A-P6
AJ281552
AJ281552.1 GI:6929432
EST.
African malaria mosquito.
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|TTTGTTTGC-AGCAGCAGATTACGCGC 1067
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GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG
                                                                                                              gcagccactggtaacaggattagcagagcgaggtatgtaggcggtgtctacagagttcttg
                                                                                                                                                                              TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA
                                                                                                                                                                                                                                                                     Anopheles gambiae pilot gene discovery project: identification mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Dimopoulos G
Fotis C. Kafatos laboratory
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//db_xref="tax/"
//db_xref="tax/"
//db_xref="tax/"
//clone="A)3A-P6FIl"
//clone="1b="Anopheles gambiae immune competent 4A3A"
//clone="lib="Anopheles gambiae immune competent / (Coll_line="immune competent 4A3A"
//cell_line="immune competent 4A3A"
//db_host="E. coli DHIUB"
//lab_host="E. coli Discord; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the forward priming site which reads from the 4A3A cell line cDNA. The 4A3A is a directionally cloned and normalized cDNA. The 4A3A is a directionally cloned and normalized cDNA ibrary that was constructed from the 4A3A cell line cludy of the collidor of the A3A cell line cludy of the collidor of the A3A cell line collidor of the A3A according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
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/strain="4A r/r"
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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99.9%;
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P., Ansorge,W.,
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N., Soares,M.B
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                                                                                          gacgagcatcacaaaaatcgacgctcaagtcagaggtggcgaaacccgacaggactataa 3823
                                              aaggccaggaaccgtaaaaaggccgcgttgctggcggtttttcccataggctccgcccccct 3763
                                 AAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huckle, E., Taylor, R., Ashurst, J.L., Sanger Xenopus tropicalis EST projec Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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EST.
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AL631067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xenopodinae; Silurana.
1 (bases 1 to 718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Aaron M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                    172
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                    /dev_stage="gastrula" (stages 10.5-13 mixed)"
//lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EccRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
was oligo dT primed from 5ug of poly A+ RNA from tages
10-13 gastrulae. EccRI-NotI cut cDNA was then ligated
into pCS107 with EccRI at the 5' end and NotI at the 3'
end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGas015ell"
/clone_lib="XGC-gastrula"
/dev_ctaron="""""
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99.0%;
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Pred. No. 1.2e-159;
Pred. No. 1.3e-159;
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                                                                              Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                     AJ281616
4A3A-P8A12-F Anopheles gambiae i
gambiae cDNA clone 4A3A-P8A12, n
                                                                                                                                          Anopheles gambiae pilot gene discovery project: identificat mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
                                                                                                                                                                                            and
                                                                                                                                                                                                    Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Rol
Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W.,
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Nematoco
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AJ281616.1
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         /organism="Anopheles gambiae"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-PBA12"
                                                                    Location/Qualifiers
 /clone_lib="Anopheles
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gambiae immune
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RESULT 1 AU081124 LOCUS

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EST 30-AUG-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Cell_line="immune competent 4A3A"
/lab host="E. coli DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
a 196 c 189 g 146 t 2 others
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Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
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il: m.sakai@cc.miyazaki-u.ac.jp.
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/clone_lib="Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus"
/tissue_type="Kidney infected by infectious hematopoietic necrosis virus"
necrosis virus"
1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oncorhynchus mykiss"
/db_xref="taxon:8022"
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Best Local Similarity
Matches 673; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xenopodinae; Silurana.
1 (bases 1 to 675)
1 (bases 1 to 675)
1 Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                         GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AL636713
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TROPICALIS_SEQUENCE_ID: TNeu013j03.sp6
Sequencing primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silurana tropicalis
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                        /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TReu013j03"
/clone="TReu013j03"
/clone=lib="XGC-neurula"
/dev_stage="neurula"
/dev_stage="neurula"
/lab_Nost="Escherichia coli DH10B"
/lab_Nost="Pscherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDN
/note="Vector: pCS107; Site_1: EcoRI; Na from neurul
was oligo dT primed from Sug of poly A+ RNA from neurul
was oligo dT primed from Sug of poly A+ RNA from neurul
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI-Rt the 5' end and NotI at the 3' end."
50 a 187 c 179 g 149 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                    11.5%;
99.9%;
                                                                                                                                                                                       0;
                                                                                                                                                                                       Score 672.4; DB 9;
Pred. No. 2.1e-153;
0; Mismatches 1;
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propicalis cDNA clone
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TNeu013j03 5',
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With
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REFERENCE
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ORGANISM
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                                                                                                                                                                                                                                                                                          AL640799.1
EST.
                                                                                                                           Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project :
TROPICALIS_SEQUENCE_ID: TNeu005c22.sp6
                                                                                                                                                                                Huckle,E., Taylor,Ř., Ashurst,J.L., Zorn,A.M. and Rc
Sanger Kenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                  AL640799
AL640799 XGC-neurula
                                                                                   Sequencing primer: SP6
This sequence is from a Xenopus
constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                     Silurana tropicalis
                                                                                                                                                                                                                                                                                                               mRNA sequence.
AL640799
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                                                                                                                                                                                                                                                                                western clawed frog.
                                                                                                                                                            Hinxton, Cambridgeshire,
                                                                                                                                                                                                                          (bases 1 to 672)
/organism="Silurana tropicalis"
/db_xref="taxon:3364"
/clone="Theu005c32"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                     GI:16792930
                                                                                                                                                                                                                                                                                                                                                                                                   675
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ia; Pipoidea;
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  Site_2:
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TNeu005c22 5',
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Pipidae;
  NotI;
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Best Local
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                                                                                                                                                                    ACTCACGTT
                                                                                                                                                                                          actcacgtt 4388
                                                                                                                                                                                                               aaaccaccgctggtagcggtggtttttttgtttgcaagcagcagcagattacgcgcagaaaaa
                                                                                                                                                                                                                                                                                                         GCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
                                                                                                                                                                                                                                                                                                                    gcgctctgctgaagccagttaccttcggaaaaaagagttggtagctcttgatccggcaaac
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                                                                          AL660035 XGC-ne
AL660035 XGC-ne
mRNA sequence.
AL660035
                                                     AL660035.1
EST.
     western clawed frog.
Silurana tropicalis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Silurana
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67; Conservative
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                                                                                                                                                                    672
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                                                                                                 XGC-neurula
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ECORI-NotI cut CDWA was then
ECORI at the 5' end and NotI
187 c 173 g 160 t
                                                                GI:17674018
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99.78;
                                                                                                  Silurana
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Pred. No. 8.8e-152;
0; Mismatches 2;
                                                                                                             gd
                                                                                                  tropicalis
                                                                                                             mRNA
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                                                                                                           linear
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Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sequencing primer: SP6
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ilarity 99.7%;
Conservative
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/db_xref="taxon:8364"
/clone="TNeu040c09"
/clone="TNeu040c09"
/clone=lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/lab_nost="Pscherichia coli DH10B"
/lab_nost="Pscherichia coli DH10B"
/lab_nost="Recetor: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
/note="Vector: pCS107; Site_1: EcoRI; ARNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
52 a 187 c 173 g 159 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
TROPICALIS_SEQUENCE_ID: TNeu017h02.sp6
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Sanger Centre
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/db_xref="taxon:8364"
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AL642581 XGC-ne
mRNA sequence.
AL642581
AL642581.1 GI:
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Sanger Xenopus tropicalis EST
Unpublished (2001)
Contact: Huckle E
Sanger Centre
                                                                                                                                                                                   Sequencing primer: SP6
This sequence is from a Xenopus constructed by Aaron M. Zorn.
                                                                                                                                                                                                                            Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project:
TROPICALIS_SEQUENCE_ID: TNeu007e10.sp6
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                        Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                   western clawed frog.
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/dev_stage="neurula"
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/lab_host="Recrition of poly A+ RNA from neuser construction coll coll and set then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
187 c 172 g 158 t
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rana tropicalis
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project 2001 (10_2001)
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cDNA clone
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Sequence 2 from Patent W00177347.
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Patent: WO 0177347-A 2 18-OCT-2001;
Archer-Daniels-Midland Company (US)
Location/Qualifiers
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Qу Db	481 481	cgggcgatagaagcgcccacgctcggcgtctgcccattgggcttcggtcagctcgggaac 540	
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Qу	661 661	tttcctgcggtgtagcgcggcgagccgaaatgatgcggatcgtctcgaccggatcggggc 720	
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Qу Db	781 781	tttgccagcggtattccccgccctcgatcctatcctgaaccgtcaggtgcaacggatcgg 840	
Qy Db	841 841	cgaacacatgcacagcatcctcgaaccggatgccatgcttcttttcgttcg	
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2100	CCAGATTGACATGTTCCCAGGGGCATAACAGGCCATCAATGTAAGAGTGCAAGCGG	2041	рb
2100	atccagattgacatgttcccaggggcataacag	2041	Qy
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2040	atcgctgcgatgctcgccatcgagaccgccaagcgtcagcgcggggtattggctcgagc	8	Оу
1980	GGGCCGCATTGGCATCAGCGGCCGCATCCGGCTCGATTGGTTTTGAGAGTGAACAAGATGC	1921	Db
1980	ggccgcattggcatcagcggcatccggctcgattggtttgagagtgaacaagatgc	N	Qy
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1080	cacgcgcgcttttgaatagaagcttgcatgataacacccgccgcgtcctcaacaaaat	1021	Qy

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VERSION
KEYWORDS
SOURCE
ORGANISM

AX281868 8509 bp Sequence 1 from Patent W00177159. AX281868 AX281868.1 GI:16609119

DNA

linear

PAT 02-NOV-2001

unidentified. unidentified unclassified.

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Schmidt,T.M. and Stoddard,S.F.
Schmidt,T.M. and Stoddard,S.F.
An endogenous Ketogulonigenium plasmid
Patent: WO 0177159-A 1 18-OCT-2001;
MICHIGAN STATE UNIVERSITY (US) ; Archer-Daniels-Midland Company
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Patent: WO 0177347-A 4 18-OCT-2001;
Archer-paniels-Midland Company (US);
Location/Qualifiers
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Retogulonigenium shuttle vectors
Retogulonigenium shuttle vectors
Patent: WO 0177347-A 1 18-OCT-2001;
Archer-Daniels-Midland Company (US);
Location/Qualifiers
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Patent: WO 0177347-A 3 18-OCT-2001;
Archer-Daniels-Midland Company (US);
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/db_xref="taxon:32630"
/note="pADM291-4DS"
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regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred q 30); an attempt was made to resolve all sequencing problem as compressions and repeats; all regions

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noted:

a11

ompressions and repeats; all regions more than one m13 subclone.
Location Qualifiers

http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset

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http://ecocyc.PangeaSystems.com/ecocyc/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome.
AE008913
Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                Submitted (29-MAR-2001) Genome Sequencing Genetics, Washington University School of Park Boulevard, St. Louis, MO 63108, USA Supported by NIH grant 5U 01 A143283
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MCClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M.,

Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes,

Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L.,

Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.

Complete genome sequence of Salmonella enterica serovar Typ
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Bacteria; Proteobacteria;
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complement(843. 1190)
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/note="STM4523"
complement(843. 1175)
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                    JOHPA-WALL COMPANY

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ILKAFPKHKIHANIIILLLIIAAAIIIFGIFNKKEKMTITIDKEKYHAIEQKTKIKPEK
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/codon ---
                                                                                                                                                                             complement (2808.
                                                                                                                                                                                                                                                        complement(2808.
                                                                                                                                                                                                                                                                                                                                                                                 QKVIAEKLDTLLAQVDSTKARLEQIPQILKRFRQSVIVAAVNGQLTKELHKKNKFKLT
ELNISIPSLWKISEIGQFADVKGGKRLPKGESLIAENTGFPYIRAGQLKNGTVLPEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        YLGKCNFETKKWSEVKKGFTQFQNDDVIFAKITPCFENGKAVVIKEFDNGYGAGSTEY
YVLRSINGLINPHWLFALVKTKDFLTNGALNWSGSVGHKRVTKEFLENYGVPVPPLAE
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                                                                                                                                                                                                                           /gene="hsdM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MSGGKLPEGWATSTINEMCNLNPKLKLDDDLDVGFMPMAGVPTT
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/product="DNA methylase M, host modification"
                                                                                                                                                                                                       /note="STM4525"
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                                                                                                                                                                                                                                                        .4408)
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o AAC77303.1 (132 aa), 79%
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NKAIJEMPTGTDETGKTGFÄDYVLFIGLKFIAVVEAKKKNTDVSSKLNESYRYSKYED
NGFLRDTLLEHYARDEVIDAVERYELISMQDTGSKQRRKIFECYSTKGREYRAMKTKS
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YDGIVVEBAHRGYILDKEOFEGELOFRSQLUDVSAYRRILDHEDAVKIALTATRALHT
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PROLITRKGLEVELOEWEDROHFEESSLASAMKATRNEDIAARLIGHTRRANGDALAGAVING
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/note="STM4527"
8249. 8254
8249. 8254
/note="mnr"
/note="mnr"
/note="mnr" RegulonDB:STMS1H004395"
8262. .9176
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complement(4555, 8084)
/gene="hsdR"
/note="STM4526"
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                                                                                                                                                   /gene="mrr"
/note="Ortholog of E. coli restriction of methylated adenine (AAC77307.1); Blastp hit to AAC77307.1 (304 77% identity in aa 1 ~ 304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="hsdR"
/note="Putative RBS
8249. .9176
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RTFDDNLDSVLDKFSDYIWDELA"
COMplement(8079. .8084)
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FTEQHLQPFETVYGEDPHGLSPREEGEWSFNAEESEVADSEENKNTDQHQATSRWRKF
SREWITRSAKSDSLDISWLKDKDSIDADSLPEPDVLAAEAMGELVQALGELDALMRELG
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/db_xref="GI:16423092"
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LTELVSYNDALDWYNGNIGKSRDDFGDMYEGLLQKNNNETKSGAGQYFTERPLIKTII
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VQSQAELEAQQQRLVALNGYIAILEGKQQETEAQTKARLAALEAQLAAKDAELAKQTE
QEKKAYHKEITDQAVKTTLELNEEESKELIDAQLKKAGWQADSKTLRFAKGARPEPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="endonuclease R, host restriction"
/protein_id="AAL23344.1"
/db_xref="G1:16423093"
/translation="MNKSNFDFLKGVNDFIYAIACAAENNYPDDPWTTLIKMRMFGEA
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/FC_number="3.1.21.3"
/FC_number="3.1.21.3"
/FC_number="0.1.21.3"
/note="0rtholog of E. coli host restriction; endonuclease
R (AAC77306.1); Blastp hit to AAC77306.1 (1188 aa), 91%
identity in aa 20 - 1188"
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/protein_id="AAL23345.1"
/db_xref="GI:16423094"
                                                                                                          /transl_table=11
                                                                                                                                       /codon_start=1
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4.1™
                                                                 methylated adenine"
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gene gene RBS

/translation="MAVPTYDKFIEPVLRFLATRPEGALVREVREAAAEMLGLDEQQR

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KEYWORDS
SOURCE
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Best Local
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            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cctttcctgcggtgtagcgcggcgagccgaaatgatgcggatcgtctcgaccggatcggg
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      Parry.C., Quail.M., Rutherford.K., Simmonds.M., Skelton.J., Stevens.K., Whitehead.S. and Barrell.B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CTI8
Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete chromosome;
AL627284 AL513382
AL627284.1 GI:165056
                                                                                                                                                       Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P.,
                                                                                                                                                                                                                                                  Parkhill,J., Dougan,G., James,K.D., Thomson,N.R., Pickard,D., Wain,J., Churcher,C., Mungall,K.L., Bentley,S.D., Holden,M.T.G., Sebaihia,M., Baker,S., Basham,D., Brooks,K., Chillingworth,T.,
                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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SHFACDFNGVKLSKLADAVALDPQPESIEDDELARSSPDDRLEQALNEIRESVAEELL
ENLLQVSPARFEVIVLDVLHRLGYGGHRGDLQRVGGTGDGGIDGIISLDKLGLEKVYV
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serovar Typhi (Salmonella typhi)
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Pred. No. 2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Location/Qualifiers
/note="Similar to Neisseria meningitidis putative periplasmic protein NMA0993 TR:CAB84263 (EMBL:AL162754) [Periplasmic protein NMA0993 TR:CAB84263 (EMBL:AL162754) [160 aa and Neisseria meningitidis hypothetical protein NNM0783 TR:AAF41196 [EMBL:AE002432) [159 aa) fasta scores: E(): 1.5e-12, 34.4% id in 160 aa. Also similar to Haemophilus ducreyi hypothetical protein TR:AAF33778 [EMBL:AF219260] [149 aa) fasta scores: E(): 9.2e-11, 31.5% id in 146 aa and Treponema pallidum hypothetical protein TP0895 TR:083865 [EMBL:AE001259) [168 aa) fasta scores: E(): 6.9e-09, 33.6% id in 134 aa. Contains a probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="STY4859"
//gene="STY4859"
/note="N-terminus is similar to Salmonella typhimurium /note="N-terminus is similar to Salmonella typhimurium IICA iicA TR:Q9RPB6 (EMBL:AF164435) (74 aa) fasta scores: E(): 3e-27, 98.6% id in 74 aa, indicated by promoterless reporter gene insertion to be induced upon bacterial invasion of phagocytic and nonphagocytic cells (but having no affect on virulence). The adjacent 70 aa is highly similar to the neighbouring CDS Salmonella typhimurium hypothetical protein TR:Q9RPB5 (EMBL:AF164435) (70 aa) fasta scores: E(): 1.9e-20, 91.4% id in 70 aa"
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LACSIYYLTERSIFFLTQRAEEDGVAP"
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DDRAMRQTLEKRPRVQCKMYDARHGFCDADSAIFDAALSHQVMDDVSAFIRDITCANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3051...3716)
/gene="STY4861"
complement(3051...3716)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Similar to Bacillus subtilis hypothetical protein YCZH YCZH_BACSU (031482) (185 aa) fasta scores: E(): 7.4e-16, 31.4% id in 159 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSTILKPFLSAVTLMLILIRPGFATEDGAITMVKTYSAYDYLQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative exported
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3375. .3404)
/gene="STY4861"
/note="PS00120 Lipases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Similar to Escherichia coli uxu operon /note-"Similar to Escherichia coli uxu operon /note-"Similar to Escherichia coli uxu operon /note-"Similar to ravus SW:UXUR_ECOLI (P39161) (257 aa) fasta scores: E(): 0, 89.9% id in 257 aa, and to Erwinia chrysanthemi exu regulon transcriptional regulator exur SW:EXUR_ERWCH (09X9E0) (259 aa) fasta scores: E(): 0, 46.9% id in 256 aa. Contains helix-turn-helix motif, residues 34 to 55, score 975(+2.51 SD). Fasta hit to PDHR_ECOLI (254 aa), 32% identity in 221 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fasta hit to EXUR_ECOLI (258 aa), 48% identity in 255 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="uxuR"
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NSMLVELFRQSWQWRENNPMWLQLHSHLGDTIYRKEWLGDHKQIILAALIKKDARAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orthologue of E. coli
UXUR_ECOLI (257 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fasta hit to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="uxu operon transcriptional regulator"
/protein_id="CAD03351.1"
                  complement(4840. .58
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/EC_number="6.1.1.2"
                                                                                                                                                                                                                                                                                                                                             /note="pfam match to entry PF00392 gntR, regulatory proteins, gntR family, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMWQHLENVKQRLLEFSNVDDIYFDGYLFESWPLDNVDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                                         complement(4840.
                                                                                                                                                                                                  signature'
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="uxuR"
                                                                                                               /note="STY4863"
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/note="Similar to Clostridium longisporum
                                                                                                                                       /gene="trpS2"
                                                                                                                                                                                                                              /note="PS00043 Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli uxuR (UXUR_ECOLI);
a), 90% identity in 257
                                                                                                                                                                                                                                    regulatory proteins,
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107.20, E-
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aa overlap"
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29508 CCTGGCCGTTTCAGCCATTCCATAACGTCGGCGTCAATACGCACCGAGGCCTGAGTTTTT 29449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 ttgctctctgcctgcatggcacgacgcaggatcgcgttcatacgggtctgatatccagac 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACGGGCGAAAAAACTTACCACGCACTGCTTCAGACCACTGTCCATCCTCCGAAGCGGGA 29389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ategggegatagaagegeceaegeteggegtetgeceattgggetteggteageteggga 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccgcccgccttgagccatgccagcacatcggcatcaagccgcgcggtgatctgctgcttg 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGAGCACTCAGCGCGGATGCGTTGCCGCGTTTATGTTTAACCATGCTCATAACGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTCGCTGTAATCAATCTCATCATCTGATTTTTTCGCCAGCGCCTTCAGTTCAGCCTCA 29329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acatcqttqgtgtcgatctgctcgggcggcagagcgtccagccgcgccaatttcttgcgg 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyctcctcggtaagagcgggcagcgtatcgaaggtgtattcaaccattggcatatctctt 658
GGTCTGCCAACGATATTCTCCATTCTCATAACGCTCCTGACGTGACAGGTGTCGGGGATC
                                                                                                                                                                                    ggtttgccagcggtattccccgccctcgatcctatcctgaaccgtcaggtgcaacggatc
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                                                                                                                                                                                                                                                                                                                        gccagcctcgatgatcaggtgggcaaccagaaggacggcagcggccatagatctgcccaac 778
                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTCTTTTCTGTCTGCCTTACGAGCGCTGATGATACGGATAACTTCAAAACCACTTTC 29209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cctttcctgcggtgtagcgcggcgagccgaaatgatgcgggatcgtctccgaccggatcggg 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tryptophanyl-tRNA synthetase TrpS or TrsA SW:SYW_CLOLO (046127) (341 aa) fasta scores: E(): 0, 54.8% id in 330 aa, and to Thermotoga maritima tryptophanyl-tRNA synthetase TrpS SW:SYW_THEMA (09WYW2) (328 aa) fasta scores: E(): 0, 36.5% id in 329 aa. Note that the E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="STY4864"
6150. .6302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trps ortholog is STY4315"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signature'
6150. .630
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synthetases class I (W and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="trpS2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="No database matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 164.8; DB 1
Pred. No. 3.5e-26;
0; Mismatches 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pF00579 tRNA-synt_1b, tRNA
Y), score 206.80, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA
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                                                                                                 898.
                              29035
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e regulator" 3743.1" 3193" PKRLILIEDDEKFAATLKRSFERRGYEV, SGLACVRALAERDPDMLIVVLTGFASIA: EGDIDAAIGGRATSIKNLEWERIHOTLV! "	CDS complement(10141547) /gene="CC176" /note="1dentified by match to protein family HMM" /note="1dentified by match to protein family HMM"	/Transi_cdote=11 /product="conserv /protein_id="AAK2 /protein_id="AAK2 /db_xref="01:1342 /translation="MAC RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAKLRGG RDLAWFNCAIDAWI RDLAWFNCAIDAWI TKVALIYKTGNLRACG TKVALIYKTGNLRACG TKVALIYKTGNLRACG TKVALIYKTGNLRACG	/codon_start=1	/organism="Caulo /db_xref="taxon: e complement(105. /gene="CC1766"	TITLE Direct Submission JOURNAL Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA FEATURES Location/Qualifiers Source 1.,10661	661) dblyum,T.V., Paulsen, Alley,M.R.K., Ohta,N. on,A., Stephens,C., I R.T., Dodson,R.J., Di R.T., Smit,J., Cran ck,T., Tran,K., Wolf te,O., Salzberg,S.L.,		RESULT 8 ABO05851/c LOCUS LOCUS ABO05851 LOCUS DEFINITION Caulobacter crescentus section 177 of 359 of the complete genome. ACCESSION ABO05851 ABO05673 VERSION KETWORDS SOURCE Caulobacter crescentus ORGANISM Caulobacter crescentus Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;	Db 29034 CTTGTTCGCATCCCATTCAAACTCCATCGGCATG 29001
CDS	gene	·	gene CDS			gene CDS	gene CDS		

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VAPYFVDADGAPNPGGWPRGGLTVVRFPNSHLIYALTWFALALFSAGAAAYVLADARR
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/gene="CC1769"
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RYKLWGYLWREWLTSVDHKKIGVMYIILALIMLLRGFADALMMRAQQAMAFGDATGYL
                                                                                                                                                                                                                                                                                                                        complement(4632.../gene="CC1772"
/note="identified
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/gene="CC1769"
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/gene="CC1770"
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PIIAESTLKQGIHNILDNALEASGSALRLSAATRDGWIRIVVEDDGPGFTSEALADFG
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/protein_id="AAK23744.1"
/db_xref="GI:13423194"
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/transl_table=11
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CGGCACATCTGGGGGATACGGCAGCAGTTGAAGGCGAACCGGGGGGGTCCGCGACCTCGCG
                                              gaccagattgccctgatccgtctcatcctgcgccaggaacgggcgtggcgggatctggct 1309
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AVLVMASLFVGEFARTGWLAY PPLSNIAYSGCVGUDYYIMALOJAGVGTLLGSINLVV
TIVKMRAPGMSLMKMPVETWTALCTNVLIVAAFPLLTAVLGLLSADRYLGTNFETNDF
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SYIVWLHHFFTMGSGASVNAFFGITTMIISIPTGAKIFNWLFTMYRGRIRFEVPMLMF
VGFMVTFVJGGWTGVLLAIPADADFVLHNSLFLIAHFHNVIIGGVVFGMFAGIVVFFFK
AFGFRLDFFWGKLSFTWFMLSGFYFAFWDLYLLGLGMGVTRTVSHFEDDSJQIMFVIAAF
GANULTLGIIAFIVQIVVSIRNREALRDETGDPWDGRTLEWSTSSFPPAYNDAFTPMV
HDLDAWNDMKQRGYVRPTSGFIFIHMFANTGAGVVLAGLSVVCGFAMIWHIWWLAVLS
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complement(6648. .7709)
/gene="CC1773"
/note="similar to PID:673470 PID:673471; identified
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIIILGAVTWSSTHLLDPYRPLDRIAPGRSAEMIKPLKVQVVALDWKWLFIYPELGIA
TVNEMAAPVDRPLNFELTSSSVMNSFYVPALAGQIYAMPGMKTKLHAVINKPGQFEGF
SANYSGDGFSHMRFKFHGMSEADFKRWVDGVRAGSGRLDRSKYLDLERRSEKQPVLRF
ASVDSGLFGAAVDRCVEPGKMCHHDMAAIDARGGLGMAGVYNVTTLEYDKRTRRGEGG
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/translation="MRYRESSPLSSRALKSLILAPAVLALGGCDWVVMNPSGDIAAQQ
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7920. .9260
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7920. .9260
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FDFFVYAIASVLVFPOLVFPFVDRLTGVMLAFGLFALAFIARPFGSVIFGAIDQRYGR
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LNAPENKRGWYAMIPQLGAPFGFMLASGLFAYFVATLAPADFLJWGWRYPFFAAFAIN
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/gene="CC1774"
/note="identified by match to
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TVFPLSWVVLHGDAQQALNFLRIELFGALVGVGGILASGWIADRITRQNQLALSALLI
GAFSLLAPRLLDGGATGQTAYVVIGFAILGLSFGQAAGAVSSGFSKKYRYTGAALTSD
LSWLIGAGFAPLAALGLASLWGLPAIGLYLASGALATULALTIDRTRRRQAHC"
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/protein_id="AAK23750.1"
/db_xref="GI:13423200"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atccgctggtcccacacccaccttagcgagagccagctgtggcgcctgttcaagtcctgg 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcacggaggtatcacctctaacc 1812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGAGCAAATAGATCTCTAGCC 103
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Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P.,
Barnett, M.J., Fisher, R.F., Jones, T., Galibert, F., Gouzy, J.,
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Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.F.
Nucleotide sequence and predicted functions of the entire
Sinorhizobium mellioti pSyma megaplasmid
proc. Natl. Acad. Sci. U.S.A. 98 (17), 9883-9888 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete plasmid sequence
AE007289 AE006469
AE007289.1 GI:14524175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE007289 12903 bp DNA lines
Sinorhizobium meliloti plasmid pSymA section 95
                                                                                                                Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P., Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P., Galizy, Hubler, F., Bowser, L., Capela, D., Galibert, F., Gouzy, J., Gurjal, M., Hong, A., Huizar, L., Hyman, R.W., Kahn, D., Kahn, M.L., Kalman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R., Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinorhizobium meliloti.
                                                        Submitted (29-MAR-2001) Biological 371 Serra Mall, Stanford, CA 94305,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                   Sciences,
, USA
                                                                                        Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 121 of the
                                                                                                                                                                                                                                                                                                                                  and Long, S.R.
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gene
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                                                                                                                                                                                                                                                                                                                                                                                         /gene="SMa1872"
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797...2122
                                                                       ryridoxai-phosphate dependent enzymes. Similar to D72386 mail as threonine dehydratase catabolic - Thermotoga mail that (strain MSB8). ACCESSION D72386 martina (strain MSB8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDPTPÖÖLRFAPÖFLPMFVKRWRSLAPGGLEGFRSGHETLVRWRLDAPTPMERMRILD PAVDNATIRLTHSRALDLLPALKNTRITAAWAGYIDSTPDGVPGIGEIAAIPGFILAA GFSGHGFGIGGFAGHLIADIVTGSEPIVDPHPYHPDRFGKSAWGKVADF" 2321. .3349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SMa1871"
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activator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="Miscellaneous; Not classified regulator"
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REGULATORY Protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:382"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SMa1869"
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                                                                                                                                                                                                                  Contains motif similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similar to C69066 339
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                                   gene
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                                                                                RGDRRQG"
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Reverse transcriptase (RNA-dependent DNA
polymerase)Similar to AAB86996 431 aa reverse
transcriptase-like protein [Shigella flexneri]. ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5568.
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/note="glimmer prediction.
integrase/recombinases."
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4616. 4957
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/protein_id="AAK65688.1"
/db_xref="GI:14524179"
                                                                                                                                                                                                                      transposases,
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translation="MAENALTAVIQEAYIQGISTRSVDDLVKGHGYEWHLQEPGQPAV
                                                                                                                                               /transl_table=11
                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                        /note="glimmer prediction, local similarity to
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                                                                                                                                                                                                                                                                                                                            function="Elements of external origin; Transposon-related
                                                                                                                                                                                                                      likely non-functional"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4584
                                                                                                                                                                                                                                                                                            1658 cgccgaaccttccccagccacatctaccgcgagaccggcaatctgcgcgccgcacagctg 1717
                                                                                                                                                                                                                                                                                                                                            4745 GTCGAAAGATGGGTGTCCAGCATCGGGCTTGATCCCAAACGCTACGGCACGCATTCAATG 4804
                                                                                                                                                                                                                                                                                                                                                                1598 ttcaagtcctggctcgagaaggcgcggctcgattcccagcctctacgggctgcactcgctg 1657
                                                                                                                                                                                                                        1718 ctgctgggccatgccagcatcgagagcaccaaggagtacatcggcaccgagcaagccgag 1777
                                                                                                                                                                                                                                                                         4805 AGGCGAACGAAGGTGGCACACATCTACAAGAAGACAGGCAACCTGCGCGCCGTCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGACCTGGCGCTGTTCAATCTCGCGATCGATAGCAAATTGCGGGCTTGTGATCTCGTC 4523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgggatctggctctgttcaacgtggcgatcgacaccagttttgcgcggctcggacctcgtg 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgcctgcgcgtctcggatgtggcgaccccagctggtctgcgtgagatcgtcgagatccgc 1417
                                                                                                                                                                                                                                                                                                                                                                                                               CTGTTTCCGAGCCGCGTGCACACAAAGCCGCATCTGTCGACGCGGCAATATAGCAGGGTT 4744
                                                                                                                                                                                                                                                                                                                                                                                                                                            accggacagggcatccgctggtcccacacccaccttagcgagagccagctgtggcgcctg 1597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGGGAGGCTGTCGGCGCATGGATTGAAAGTCGCAGACTCGGTGAAC----GGGATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGCTAGGCCACAAGAAGCTGGAGAGCACCGTACAATACCTCGGAACCGAGGTGGACGAC
                                                                                                                                                                   gecetegatatege 1791
                                                                                                                                      GCCCTGGCCATCTC 4938
AC098576 101711 bp
Drosophila melanogaster chromosome
SEQUENCE, 17 unordered pieces.
AC098576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="Miscellaneous; Not classified regulator"
/note="glimmer prediction. Similar to AE004024_1 205
transcriptional regulator (ACTR family) [Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(9113. .9772)
/gene="SMa1882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical protein"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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NRS Muzny, D.M., Adams, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S.L., Amarratunge, H.C., Are, J.R., Ngyel, M., Banks, T., Alsbrooks, S.L., Amarratunge, H.C., Are, J.R., Ngyel, M., Bryant, N. P., Barbaria, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Blange, K., Blown, E., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burbaria, J., Bowie, S., Brown, E., Brown, M., Bryant, N.P., Chen, R., Ch
Worley, K. C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alams, C., Adams, C., Are, J.R., Banks, T., Barbaria, J., Blashcoks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bornin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, C., Harris, K., Hart, M., Haylak, P., Haue, S., Hamilton, K., Harris, C., Hodson, A., Hogues, M., Hollows, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L., Liu, J., Liu, W., Lewis, L., Liu, W., Lewis, L., Liu, J., Liu, W., Lewis, L., Liu, J., Liu, W., Lewis, L., Liu, W., Lewis, L., Liu, W., Lewis, L., Liu, W., Lewis, L., Liu, R., Lucier, R., Luna, R., Lucier, R., Lucier, R., Luna, R., Lucier, R., Lucier, R., Lucier, R., Lucier, R., Lucier, 
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Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L. L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Raiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Walli, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Warli, S., Ward-Moore, S., Warren, R., Washington, C., Weinstock, G., and Glbbs, R.

Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 4, 2002 this sequence version replaced gi:17933776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator Big Dye: 99% of reads Assembly program: Phrap; version 0,990329
Consensus quality: 91258 bases at least Q40
Consensus quality: 93289 bases at least Q30
Consensus quality: 9526 bases at least Q30
Estimated insert size: 149230; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 4.3x in Q20 bases; sum-of-contigs estimation
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Center clone name: RP98-3E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Best Local :
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                                                         CAATAATGTATCATAAATTTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acatcgttggtgtcgatctgctcgggcggcagagcgtccagccgcgccaatttcttgcgg 598
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                                                                                  tagttattcaatggcaagtcgca
                                                                                                                               cgccttggcgggatcccagataaaccgcatcttcatggcagaattataactacacatttg 955
                                                                                                                                                                                                                                                            aacggtttgccagcggtattccccgccctcgatcctatcctgaaccgtcaggtgcaacgg 835
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                                                                                                                  ATTCTTTGCCTCATCCCATTCGAAATACTGTTTCATAAAAAACATTCAAATTTGTATATA 48484
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/db_xref="taxon:7227"
/chromosome="X"
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AF429315
AF429315.1 G
                                                                                                                                                                                    gcggctcggacctcgtgcgcctgcgcgtctc-ggatgtggcgaccccagctggtctgcgt 1399
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                                cgcctgtcggaggggacacgcgagagcctgcgggtctatctcgcggcctctgacaagccg 1519
                                                                                                      gagatcgtcgagatccgccagaagaagaccgaggcccgcaatgtccgccccgtacaggcc 1459
                                                                                                                                                              CCCCCTCTGAACTTACCCCCCTGTGGGACCCAGGTAGTAGCGGCCATCGCARRKMMKSHA 16882
GMCCWGRRRSKGWKWYSRGMSRSKSMRYTGGSK-
                                                                                 GRRRMCYYSKSWMSMBMSVSYSVKMHSMHASBSCMHWBKCMTWSCCMSMMYKSSWWGSSW
                                                                                                                                                                                                                                                                                                                             154;
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I (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang Ingersoil-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A Potter, N.T., Ross, C.A. and Margoils, R.L. A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medica Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Holmes, S.E., Ingersoll-Ashworth, R.G.,
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/gene="JPH3"
/product="junctophilin 3"
complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
/tdb_xref="GI:17646245"
/translation="MSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS/
HGFEVLGVYFRPSGNTYGGTWAAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
1 32731 c 30696 g 28283 t 4254 others
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                             401;
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Pred. No. 0.00028;
1; Mismatches 443
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    -MMRSSMMCTSSCYASMCCMC
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RESULT 1 AE000070 LOCUS KEYWORDS SOURCE DEFINITION REFERENCE REFERENCE VERSION ACCESSION JOURNAL MEDLINE TITLE AUTHORS ORGANISM AE000070 9973
Rhizobium sp. NGR234 plasmid complete plasmid sequence.
AE000070 U00090
AE000070.1 GI:2182363 97305956 2 (bases Molecular basis of symbiosis between Nature 387 (6631), 394-401 (1997) Freiberg, C., Fellay, R., Rhizobiaceae; Rhizobium.
1 (bases 1 to 9973) Rhizobium sp. NGR234. Rhizobium sp. NGR234 and Perret, X. Bacteria; Proteobacteria; 1 to 9973 Bairoch, A., alpha subdivision; pNGR234a, dq DNA Broughton, W.J., Rhizobium section linear tion 7 c Rhizobiaceae of BCT 12-DEC-1997 46 of the group;

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Broughton,W.J. and Perret,X.P.
GENOMIC SEQUENCE OF RHIZOBIUM SP. NGR234 SYME
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                                                Mammalia; Eutheria; Primates; Catarrihin; Viammalia; Eutheria; Primates; Catarrihin; Viammalia; Eutheria; Primates; Catarrihin; Viammalia; Eutheria; Primates; Catarrihin; Viammalia; Eutheria; November, R., Rosenblatt, A., Catarrihin, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgatgctcgccatcgagaccgccaagcgtcagcgcgggtattggc 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGAACCAAGGGACAGATGATGGTCCATCATTTCGGCCAGGAAGAGGATGCGGTCCGAT 83743
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125; Conservative
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Sequence 1 from Patent WO9802560.
A93002
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1 (bases 1 to 320040)

1 (bases 1 to 320040)

Broughton,W.J. and Perret,X.P.

BROUGHTO.SEQUENCE OF RHIZOBIUM SP. NGR 234 SYMBIOTIC PLASMID GENOMIC SEQUENCE OF RHIZOBIUM SP. NGR 234 SYMBIOTIC PLASMID PATENT: WO 9802560-A 1 22-JAN-1998;

PIOLOC MOLECULAIRE DES PLANTES (CH); BROUGHTON WILLIAM JOHN (CH)

LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
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                                                                                                                                                                                                                                                                                                                                                                                        125020 bp
Homo sapiens junctophilin 3 (JPH3)
AF429315
AF429315.1 GI:17646244
                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata;
Entaryota; Metazoa; Primates;
                         11694876
  (bases 1 to 125020)
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/db_xref="taxon:32644"
93201 c 94558 g 66028
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Pred. No. 0.0019;
0; Mismatches 100; Indels 0
                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                       junctophilin-3 is
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partial cds
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%; Score 62.6; DB 9; Length 1 Best Local Similarity 9.3%; Pred. No. 0.0059; Matches 83; Conservative 394; Mismatches 416; Indels
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1625 ctcgatcccagcctctacgggctgcactcgctgcgccgaaccttccccagccacatctac 1684
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                                                                                                                                             ccagctggtctgcgtgagatcgtcgagatccgccagaagaagaccgaggcccgcaatgtc 1444
                                                                                                                                                                                                                                                                                                                                                              SYWKCCAKWWMSYCCWSYCMTYYYSKSCTYKSSTCYKRGGYYWGSKTCYSAGGKSRSMYY 17544
                                                                                                                                                                                                                                                                                                                                                                                                                                               YSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRKRSYYYWGGGKRAKKKYYCAGRRRRM 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atccgtctcatcctgcgccaggaacgggcgtggcgggatctggctctgttcaacgtggcg 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggaacaagggccgcgttgtcgggaaaaagccgccgctgacacctgaccagattgccctg 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRGSMSSKGWRGYAGRGCYSSSMWSTRKRRSKCYSYKSYKKGRGKMKGWGGMKRGSKYWS 1730
                                                                               acccaccttagcgagagccagctgtggcgcctgttcaagtcctggctcgagaaggcgcgg 1624
                                                                                                                      CCMKKKGCTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWGYSWMKCMKYMSYKKKRRS 1736
                                                                                                                                                                                                   GSYGSTGRSMKKKKGYSKYSRGMKGKKKTCYCMWKYYKYRKTSMCWWYYMKSWGYKRYKR 1742
                                                                                                                                                                                                                            CMMRSSKSSSWSMSMARSSWCMGWGAGYRRSKRSAGWGAGWRSSKGKRSTGMKRACSKKT 17484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \label{eq:holmes} \begin{subarray}{ll} Holmes, S.E., & Ingersoll-Ashworth, R.G., & Ross, C.A. & and & Margolis, R.L. \\ Direct & Submission \\ \end{subarray}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<36507. .36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="junctophilin 3" complement(<36507. .>36887)
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membrane and endoplasmic reticulum"
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/db_xref="taxon:9606"
/chromosome="16"
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                                                                                                                                              1925
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                                           1985 gctgcgatgctcgccatcgagaccgccaagcgtcagcggggtattggctcgag 2038
                                                                                                                                                                                                                       taccgcatggcggtcctgccgaacctgttcggggaatggacgctgtatcgagaatggggc 1924
                                                                                                                                                                                                                                                                                         GWGRKGRKCMSSRKMKMYKSYYRRKRWMTCMKMCYSMYMAMYCRSMCCMCMCKSCCGCYS
                                                                                                                                                                                                                                                                                                                                                                                                                                accaaggagtacatcggcaccgagcaagccgaggccctcgatatcgcacggaggtatcac 1804
KCWSSCWWSSMRKKSKGGSWAKGMVWDKGSVSTDKSDKMBSRSBSKVKSKWSMS 16891
                                                                                             SYKGGGSWGGKGGKSTRGSSAGKKSSYKKMSCCARYKSMSYSKCYSRWMWCMSYYYCWGG
                                                                                                                                         cgcattggcatcagcggccgcatccggctcgattggtttgagagtgaacaagatgccatc
                                                                                                                                                                                         MGMSSYSYSGKYSWGMKSYM-WRSYYSKRSTSKAWRSSKRGMGTGGRYKGGGRSYGKGGG
                                                                                                                                                                                                                                                                                                                                       ctctaacccatggagacctatctcgagaagcgcatccccgccaagaacacagcacggttc 1864
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Search completed: August 20, 2002, 13:00:12 Job time: 22660 sec

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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Perfect score:
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Match
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Listing first 45 summaries
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ALIGNMENTS

RESULT AA167035 New nucleic acid comprising the sequence of a Ketogulonigenium plasmid designated pADM291 is endogenous to microorganism strain NRRL B-30035 $\,$ WPI; 2001-657165/75. 05-APR-2001; 2001WO-US11058 AAI67035 standard; DNA; Schmidt TM, (UNMS) UNIV MICHIGAN STATE. 05-APR-2000; 2000US-194624P WO200177159-A2 Synthetic Ketogulonigenium; plasmid; strain NRRL B-30035; vector; ds. Nucleotide sequence of an endogenous ketogulonigenium plasmid 11-FEB-2002 AAI67035; 18-OCT-2001. (first entry) Stoddard 8509

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                                                                                                                                                                                                                                    The present invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, pADMJ91. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coli, enable the cloning of certain genes of Ketogulonigenium in E.coli as the latter is an efficient host for amplification of vector DNA. The present DNA sequence represents the Ketogulonigenium endogenous plasmid pADMZ91.
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	ag 6360 ag 6360	ttaggatgaatctgtccggctcttgacataccccgcgtgaaaccctgtctttacaaga 	Qy 630 Db 630
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_	ta 6240 ta 6240	ccgctgatattccaccaaggtgagtcctgtagatcagactctcaaggagtaaacgtttt 	Qy 618
	ac 6180	ttgtggcggatttcaacctcaaaacagatggtatttgaatgtcaggacaggtgaaatca 	Qy 612 Db 612
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   2002-049150/06
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rmed host cell; Escherichia coli; plasmid vector replica
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Novel nucleic acid vector comprising Ketogulonigenium replicon found a specific deposited endogenous plasmid, useful for producing polypeptides and/or transcripts by culturing host cells transformed with vector -

Claim 4; Fig 4; English

The present invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, pADM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coll, enable the cloning of certain genes of Ketogulonigenium in E.coll as the latter is an efficient host for amplification of vector DNA. The present DNA sequence represents the region of Ketogulonigenium endogenous plasmid pADM291 that supports plasmid vector replication.

Sequence 2517 BP; 657 A. 589 C; 683 <u>.</u> 588 Τ; 0 other;

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Gaps

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Length Indels

Ωy Qy Вb δõ Вþ Ωy g Qy 밁 B 망 Qy Вb Qy B Q Вþ δÃ DЪ QΥ Query Match
Best Local Similarity
Matches 2517; Conserv 3075 3015 2955 3495 121 181 421 301 241 361 481 61 ctgcgcggagatctctggttctcaggtagggcgacaatggagaggtgttagttgccccctg 3074 ctgcgcggagatctctggtctcaggtagggcgacaatggagaggtgttagttgccccctg gattactgatagtttctgcctgtcgggcttgtcgggcttgtcgggcttgtc gattactgatagtttctgcctgtcgggcttgtcggggcttgtcggggcttgtcggggcttgtc tatcgctctctgcgtggcgcattgggtcatcctgcccggacatatgatattccgctagag tatogotototgogtggogoattgggtoatoctgoooggacatatgatattoogotagag 3134 aattgggccgcaaaagggagtaattgggccgatatcggttgtttacatggggaggaatcc attcgcttaaaagggagtaattgggccgcaaaagggagtaattgggccgcaaaagggagt ccttcttgttctatagttcttatagttcatacgaaaattacacataattatcaatagctt ccttcttgttctatagttcttatagttcatacgaaaattacacataattatcaatagctt attcgcttaaaagggagtaattgggccgcaaaagggagtaattgggccgcaaaagggagt aattgggccgcaaaagggagtaattgggccgatatcggttgtttacatggggaggaatcc gatgatgtgcgccatgaaatgcggctggccgacattcgcgcaatcgacggcatgaaaaac cycctycayycyctcaayctcatycatttaatyatayccactycygycygccycatyyct cagacaaaaactgtgctccctgccgaggtggcgagaggggtctatatgcgcaatccgccc cagacaaaaactgtgctccctgccgaggtggcgagaggggtctatatgcgcaatccgccc ccttaatcatttctccccatgggaaagacaacaagtggccgcagaccgggccttcgac ccttaatcatttctccccatgggaaagacaacacaagtggccgcagaccgggccttcgac 29.6%; ilarity 100.0%; Conservative score 2517; D Pred. No. 0; 0; Mismatches 120 60 3014 180 3374 3314 3254 420 360 300 240 3494 480 3674 3554 540 3434

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                             gtttttttgccagagagagacacgtttttgatggtgtaataaactgctacgtatctcatg
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AAS18306;
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           standard;
           DNA;
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            ВP
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12-MAR-2002

(first

entry)

Cloning vector; F transformed host Ketogulonigenium of Ketogulonigenium replicon;
cell; Escherichia coli; p. Ketogulonigenium sp. strain replicon pADM291; ds. from plasmid plasmid;

WO200177347

18-0CT

05-APR-2001; 2001WO-US11059

05-APR-2000; 2000US-194625P

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Best Local Similarity 99.8
Matches 2010; Conservative
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The present invention relates to the isolation of vectors comprising a Ketoguloniqenium replicon found on the endogenous plasmid, pADM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coll, enable the cloning of certain genes of Ketogulonigenium in E.coli as the latter is an efficient host for
                                                                                                                      Claim
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418673...419680
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/product= "encapsulation-like protein"
/note= "homologous to the CapA gene"
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/product= "oligopeptide pe
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419677..420738
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420774..422159
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/product= "(semi)aldehyde d
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                       /product- "gamma-hexachlorocyclohexane-dechlorinase-like protein" /note= "homologous to the LinA gene" 448497. 450203
                                                                                                                                                                                       /standard_name= "ORF K22"
/product= "ferrodoxin-like protein"
/note= "homologous to the NifQ gene'
/45088...446602
                                                                                /standard_name= "ORF L1"
/product= "cytochrome P450-like protein"
/note= "homologous to the CamC gene"
/47844...448500
                                                                                                                                                                                                                                                                           /standard_name= "ORF K20
/product= "protein of unknown
complement (443313...443879)
                                                                                                                                                                                                                                                                                                                  /product= "protein required
complement (442316..442636)
                                                                                                                                                                                                                                                                                                                                                                 /product= "protein required complement (441042..441899)
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/*tag= o
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/gene= "nifB"
/product= "protein involv
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/product= "protein of unknown function"
complement (434517..434711)
/standard_name= "ORF L3"
/product= "putative protein with degradative function"
                                                                                                                               /product= "C4-dicarboxylate transport protein"
/note= "homologous to the DctAI gene"
/446599..447843
                                                                                                                                                             /standard_name= "ORF K23"
/gene= "dctA"
                                                                                                                                                                                                                                      /standard_name= "OI
/product= "protein
444337..445029
                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF K19"
/gene= "fixA"
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/gene= "fixC"
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/gene= "fixX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (438297..438590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "ORF K15"
/gene= "nifA"
                                                                                                                                                                                                                                                                                                                                                                                    /gene= "fixB"
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                                                                                                                      /*tag=
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biosynthesis"
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ttggaaccaagggacagatgatggtccatcatttcggccaggaagaggatgcggtccgat 83743
         aaccctaccggctctatgtcgagcgcctggatccctcgaggaatatggcccgctactatg
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                    /standard_name= "ORF L4"
/product= "luciferase alpha-subunit-like protein"
/note= "homologous to the LuxA gene"
452980..454494
                                                                                                                                                                                                 /standard_name= "ORF L14"
/product= "peptidase-like
/note= "homologous to the
464736...466079
                                                                                                                                                                                                                                                /standard_name= "ORF L13"
/product= "protein of unknown
463201..464739
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "homologous to the FixF 459093...459575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF L7"
/gene= "nifK"
/product= "beta-subunit of
456187...457677
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454590..456131
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                                                                                                                                                            /standard_name= "ORF L15"
/product= "processing prof
/note= "homologous to the
                                                                                                                                                                                                                                                                                                                                            /standard_name= "ORF L11"
/product= "protein of unknown 460501..460920
                                                                                                                                                                                                                                                                                                                                                                                    459579..460067
                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "ORF L10"
/product= "protein of unknown function"
/note= "homologous to the Nifx gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product=
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457687..459096
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"protein involved biosynthesis"
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12-JUL-1996;
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                                                                                                               83564 aaccctaccggctctatgtcgagcgcctggatccctcgaggaatatggcccgctactatg 83623
                                                                                                                                                                                                                                                                        This is the nucleotide sequence of the plasmid pNGR234a isolated from Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the nucleotide sequence are claimed. The nucleotide sequences or ORFS can be used e.g. in the transportation of compounds to and from an organism be used e.g. in the transportation of compounds to and from an organism which is a host to at least one of the nucleotide sequences, ORFS or proteins, the degradation and/or metabolism of organic, inorganic, natural or xenobiotic substances in a host organism or the modification natural or xenobiotic substances in a host organism or the modification of the host range, nitrogen fixation abilities; for obtaining a synthetic minimal set of ORFS required for functional Rhizobium-legume symbiosis, especially for nodulation efficiency on host plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to develop products for modifying plant characteristics, e.g. nitrogen fixation, synthesis of compounds and stress response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Broughton WJ,
                                                       (BIOL-) LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) INST MOLECULAR BIOTECHNOLOGY.
(BIOL-) LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
                                                                                                                                                 1809
                                                                                                                                                                                                                                               Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;
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                       ttggcatcagcggcccgcatccggctcgattggtttgagagtgaacaagatgccatcgctg 1988
                                                                      gcatggcggtcctgccgaacctgttcggggaatggacgctgtatcgagaatggggccgca 1928
ttggaaccaagggacagatgatggtccatcatttcggccaggaagaggatgcggtccgat 83743
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96EP-0730001
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Pred. No.
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n fixation; nodulation;
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                                                                                                                   Ax The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of movel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC genes themselves and the encoded proteins. The prokaryotes used are CC genes themselves and the encoded proteins. The prokaryotes used are CC invention is also useful for the identification of potential new targets CC invention is also useful for the identification of potential new targets to identify proteins used in proliferation, to express these proteins, to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC are proteins can be used to screen compounds in rational drug discovery CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery CC as wide variety of organisms. The present sequence encodes an accessing the protein of the printed specification, but was obtained in electronic CC of the printed specification, but was obtained in electronic cf from at directly from WIPO at the protein that protein the protein that protein the protein the protein that protein the protein the protein that protein t
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Seq ID No 7846; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotics, comprise sequences of antisense nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
Yamamoto RT,
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16-FEB-2001;
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                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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2000US-206848P
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2000US-242578P
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2000US-259308P
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Xu HH;
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Query Match Best Local Similarity

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       The invention relates to an isolated and purified nucleic acid segmer comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycipikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the produc of biologically active macrolides. The macrolide biosynthetic protein
                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asth chronic obstructive pulmonary disease; respiratory inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              narbomycin. The alternative termination of polyketide synthesis may useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are use biopolymers, e.g., in packaging or biomedical applications, to as biopolymers, e.g., packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active ages of the produced by the compound of the produced by the produ
                                                                                                                                                                                                       neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase biopolymer; antibiotic; chemotherapeutic; immunosuppressant; ast chronic obstructive pulmonary disease; respiratory inflammation;
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The invention relates to an isolated and purified nucleic acid segment cc comprising a desosamine biosynthetic gene cluster, a fragment or its cc biologically active variant, where the nucleic acid sequence is not cc derived from the eryC gene cluster of saccharopolyspora crythraea or cc streptomyces antibioticus. The invention also relates to a macrolide cc biosynthetic gene cluster, or fragments thereof. The macrolide cc biosynthetic gene cluster encodes proteins which synthesise methymycin, arabomycin or a combination of these cc pikromycin, neomethymycin or augmented cells comprising the desosamine cc compounds. Recombinant or augmented cells comprising the desosamine cc and/or macrolide biosynthetic gene clusters are useful for the production cf of biologically active macrolides. The macrolide biosynthetic proteins care useful for synthesis of methymycin, pikromycin, neomethymycin and are useful for the alternative termination of polyketide synthesis may be
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                                                                                                                                                                                                                                                                                               Sherman DH, Liu H,
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                                                                                                                                                                                                       Desosamine and macrolide biosynthetic synthesis of methymycin and pikromvcin
                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                Disclosure; Figure 32; 438pp;
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AAY77209, AAY77210
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/transl_except= (pos:8270..8272, aa:Val)
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, AAY77211, AAY77212, AAY80998, AAY80999
                                                                                                                                                                                                            pikromycin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pacteria, including multi-drug resistant pneumococci and other prespiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine polyketic gene cluster (pik) from Streptomyces venezuelae ATCC 15439, as given in figure 32.
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                                                                                                                                                   Narbonolide synthase; polyketide synthase gene; narbonolide antibiotic; Cl2-hydroxyalse; picK; desosamine biosynthesis; desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme; ketolide; beta-glucosidase
                                                                                                                                                                                                                                                                                                                                     AAA75633 standard; DNA;
                                                                                                                                                                                                                           Nucleotide sequence of the insert DNA in cosmid
                                                                                                                                                                                                                                                                 22-JAN-2001
                                                                                                                                                                                                                                                                                                 AAA75633;
                                                                                                    Streptomyces
                                                                                                                                      picromycin
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22-SEP-1998;
08-FEB-1999;
20-MAY-1999;
30-APR-1997;
06-MAY-1998;
28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is used to produce the recombinant DNA compounds of the invention. The specification describes a recombinant DNA compound expressing recombinant polyketide synthase genes in host cells for the production of narbonolide, narbonolide derivatives and polyketides that are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (pick), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    st cells are useful as genetic systems that allow rapid engine
the narbonolide polyketide synthase. These would be valuable
eating novel ketolide analogs for pharmaceutical applications.
                                                                                                                                                                                                                                                               ttggcatcagcggccgcatccggctcgattggtttgagagtgaaccaagatgccatcgctg
                                                                                                                                                                                                                                                                                                                                                                                             gcatggcggtcctgccgaacctgttcggggaatggacgctgtatcgagaatggggccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aacccatggagacctatctcgagaagcgcatccccgccaagaacacagcacggttctacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggagtacatcggcaccgagcaagccgaggccctcgatatcgcacggaggtatcacctct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agaccgtcccgtgtgtccccgtccggctcccgtccgcccatcccgccctccaccggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acggcctggtgcccctggcctgggctgctcgccgccgggcacgaggtgcgggtcgcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggaaggacacgacgccatgcgcgtcctgctgacctcgttcgcacatcacacgcactact
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                                                 ttgacatgttcccaggggcata
                                                                                                           cggcgatcgccttcgacgaggcccgtcccgagccgctggactgggaccacgccctcggca
                                                                                                                                          cgatgctcgccatcgagaccgccaagcgtcagcgggtattggctcgagcccatccaga
                                                                                                                                                                                                                                ccgaccacctcatccacgagtaccgggtgcggatggcggagccgcgcgcacccatc
                                                                                                                                                                                                                                                                                                                                                     gccagcccgcgctcacggacaccatcaccgggtccgggctcgccgcggtgccggtcggca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Betlach
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98US-0100880
99US-0119139
99US-01134990
97US-0846247
98US-0073538
98US-0141908.
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Pred. No. 0.26
0; Mismatches
                                                       2070
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,.26;
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RESULT 12
AAZ56001
28-MAY-1998;
28-AUG-1998;
22-SEP-1998;
08-FEB-1999;
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antibiotic p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ56001 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ56001
      Example
                    New recombinant DNA encoding a domain synthase, for production of ketolide
                                           P-PSDB; AAY67201, AAY67202,
AAY67208, AAY67211.
                                                                          Ashley
                                                                                                                                                                              W09961599-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces
                                                           WPI; 2000-072618/06
                                                                                        (KOSA-)
                                                                                                                                                27-MAY-1999;
                                                                                                                                                              02-DEC-1999
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      2
                                                                                          KOSAN
      Page
                                                                          Betlach MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                               venezuelae
                                                                                          BIOSCIENCES
                                                                                                         98US-0087080.
98US-0141908.
98US-0100880.
99US-0119139.
                                                                                                                                               99WO-US11814
      16-27; 98pp;
                                                                                                                                                                                                                                                                                                              /note= "Narbonolide 33961..34806
                                                                                                                                                                                                                                                 /product= PICCII
/note= "4-keto-6-deoxyglucose
36159..37439
                                                                                                                                                                                                                                                                                                                                                                                                               /product= PICAI
/note= "Narbonolide synthase subunit 1"
                                                                                                                                                                                            /product= PICCVI
/note= "3-amino (
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
70..13725
                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                   /note= "Desosaminyl
37529..38242
                                                                                                                                                                                                                                   /product= PICCIII
                                                                                                                                                                                                                                                                                              /product= PicB
                                                                                                                                                                                                                                                                                                                              /product= PICAIV
                                                                                                                                                                                                                                                                                                                                                           /product= PICAIII
                                                                                                                                                                                                                                                                                                                                                                                          /product= PICAII
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narbomycin; picromycin;
                                                                                                                                                                                            "3-amino dimethyltransferase"
                                                                                                                                                                                                                                                                                                                                                     "Narbonolide
                                                                                                                                                                                                                                                                                                                                                                                   "Narbonolide
                                                                          Betlach
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                                                   AAY67203,
      English
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                           domain of narbonolide
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                                                                                                                                                                                                                                                                                      typeII
                                                                          McDaniel
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                                                                                                                                                                                                                           transferase"
                     antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cosmid pKOS023-27; ketolide;
cromycin; ds.
                                                    AAY67204, AAY67205, AAY67207,
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                                                                         Tang
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                           polyketide
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CC Streptomyces venezuelae DNA insert. The cosmid contains open reading CC frames which encode the various modules of the narbonolide polyketide CC synthase (PKS). The invention relates to recombinant DNA containing a CC coding sequence for a narbonolide PKS. Polyketides are compounds CC synthesised from 2-carbon units through a series of condensations and CC subsequent modifications. Modular PKS are responsible for the production CC of many antibiotics including picromycin. The narbonolide PKS consists of condensations and containing module, six extender modules, and two thioester domains. Four CC proteins make up the narbonolide PKS (PICAI, PICAII, PICAII, PICAII, PICAII, PICAII, PICAII, PICAII and PICAIV). CC proteins make up the narbonolide PKS (PICAI, PICAII, PICAII and PICAIV). CC proteins make up the narbonolide PKS (PICAI, PICAII, PICAIII). PICAIII and PICAIV). CC proteins make up the narbonolide and extender modules 1 and 2, PICAII are protein includes extender modules 3 and 4, PICAII includes extender module 5 and cc picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes extender module 6 and a type II thioesterase domain. The CC picaiv includes
RESULT 13
AAH41175
ID AAH4111
XX
AC AAH411
XX
DT 23-AUG
XX
XX
Mammal
XX
Mammal
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Best Local Similarity
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                                                                                                                                                                                                 AAH41175
                                                                                                                                                                                                                                                             AAH41175 standard;
                                                                                                                                  23-AUG-2001
                                                                  Mammalian Cre recombinase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aggaaggacacgacgccatgcggtcctgctgacctcgttcgcacatcacacgcactact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttgacatgttcccaggggcata 2070
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                                                                                                                                  (first entry)
          recombinase; organ transplantation; gene therapy;
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45.3%;
                                                                                                                                                                                                                                                                DNA;
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Pred. No. 0.
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RESULT 14 AAA10594

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Best Local Similarity
Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a mammalian type Cre recombinase gene. This sequence can be modified so as to have a high expression efficiency mammal by selecting a codon of high frequency for use in the mammal expressing Cre recombinase. The gene can be used in organ transplantation, gene therapy and creation of animal disease models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian type Cre recombinase gene modified so as to have a high expression efficiency in a mammal by selecting a codon of high frequency for use in the mammal for expressing Cre recombinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-360321/38
P-PSDB; AAB98695.
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atggcccgcgccggcgtgagcatccccgagatcatgcaggccggcggc
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                                                                                                                                                                                                                        aagctggtggagcgctggatcagcgtgagcggcgtggccgacgaccccaaccactacctg
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                 ctgctgctgggccatgccagcatcgagagcaccaaggagtacatcggc 1762
                                                      agcggccagcgctacctggcctggagcggccacagcgcccgcgtgggcgccgccgcgac
                                                                                                                                 ctgttcaagtcctggctcgagaaggcgcggctcgatcccagcctctacgggctgcactcg
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                                                                                   ctgcgccgaaccttccccagccacatctaccgcgagaccggcaatctgcgcgcacag
                                                                                                             cgggccctggagggcatcttcgaggccacccaccgcctgatctacggcgccaaggacgac
                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                             thrsrrgthrrthrysa-----snthrthrggncysaavagggasnysvaysgsrasna
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                                                                                                                                                                                                                              raagvasrhsysgngngsrthrysysaaysggcysgnargargvaargysargrgyraaa
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                               asrgashshargsrgysysysgrsrcysyssrvagyaasrasasnmtasashvagmtgys
                                                                           hssrasnvaaasrhsghsrhaasrsrasaagysrasasysthrsrcysaagsrtraasra
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OJI PAPER CO
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                                                   /product= "NysN protein"
/note= "CDS does not include
complement (60238..61296)
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/note= "CDS does not include
complement (59045..60241)
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/product= "NysJ
51155..57355
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/product= "NysD2 complete
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complement (58786..58980)
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10-APR-2000;
14-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 188-254;
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P-PSDB; AAE10143, AAE10144, AAE10145,
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 other;
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S, Ellingsen ק
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DZIEGLEWSKA H.
DZITCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
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Gulliksen
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Search completed: August 20, Job time: 20837 sec 2002, 13:15:54

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US-08-464-517-25
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pil
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEO ID NOS: 43
SCOTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 3
; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
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ALIGNMENTS

Application

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Query Match
Best Local Similarity
Matches 173; Conserv
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Sequence 19, Application US/09320878A Patent No. 6117659

GENERAL INFORMATION:

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FILE REFERENCE: 30062202120

CURRENT APPLICATION NUMBER: US/09/320,878A

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER FILING DATE: 1998-08-28

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER FILING DATE: 1997-04-30

EARLIER FILING DATE: 1997-04-30

EARLIER FILING DATE: 1999-09-08

EARLIER FILING DATE: 1999-09-08

EARLIER FILING DATE: 1999-09-08

EARLIER FILING DATE: 1999-09-08

EARLIER APPLICATION NUMBER: 60/10,880

EARLIER APPLICATION DATE: 1998-09-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
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TYPE: DNA
ORGANISM: Streptomyces venezuelae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE: CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                  1397
                                                                                                                                                                                                                4548
                                                                                                                                                                                                                                          4488 atagtgttaaatgactttcgtgaaacgatgtgcaatatagcggtaagactatgaaataca 4547
                         4728 tatatggtaagcgtgatgaaacacatgaaatgacctcagaaatcagcgcattagagcgtg
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CITY: Alexandria
                                                                                                                                                                                                                                                                                                y Match 0.5%; Score 45.8; DB 1; Local Similarity 3.8%; Pred. No. 0.037; hes 14; Conservative 205; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                      aattgcacagagtgtttcctcccatttcaaagaaatacaccgaaacacctaacacgcaag
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7218 base pairs
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VENTION: RECOMBINANT FOWLPOX VIRUS
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4787 1218 4727 1278

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RESULT 4
5212296-8
; PATENT NO. 5212296
; PATENTICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO,
; J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES
.TEPPERMAN, JAMES M.
.TEPPERMAN, JAMES M.
                                                                                                                                RESULT 5
US-08-852-401-1
Sequence 1, Application US/08852401
Patent No. 5976836
Patent No. 5976836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FILING DATE: 11-SEP-1989; SEQ ID NO:8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5%;
Best Local Similarity 45.6%;
Matches 152; Conservative
                                                                                                                           GENERAL INFORMATION:
                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
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                  APPLICANT: Luu, B. Minh
TITLE OF INVENTION: Met)
TITLE OF INVENTION: Ery
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                                                                                                                                                                                                                                                                                                                                                                                                                   ogcggctcgatcccagcctctacgggctgcactcgctgcgccgaaccttccccagccaca 1679
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                                                                                                                                                                                                                                                    acaacggcgttccccggatcgccaccgaggacg 1092
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                                                                     Hessler, Paul E.
Larsen, Peter E.
                                                                                                          Weber, J. Mark
Methods and Compositions for Enhancing Erythromycin Production 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43.4; DB 6; Length 1998;
Pred. No. 0.078;
0; Mismatches 181; Indels 0
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US-09-082-092-15

: Sequence 15, Application US/09082092

: Patent No. 6251628
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: Nakao, A
APPLICANT: Moren, A
APPLICANT: Heuchel,
APPLICANT: Itoh, Su
APPLICANT: Afrakhte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: FETELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4776 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa L.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 1679 atctaccgcgagaccggcaatctgcgcgccgc 1710
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                                                                         APPLICANT:
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NUMBER OF
                TITLE OF
                             APPLICANT:
                                          APPLICANT:
                                                            APPLICANT:
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STATE: Illinois
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STREET: 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                               ATCTACCGGGAGTGGCGCGAGCTGCTGGACTC 2649
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         INT: Landstrom, Marene
INT: Heldin, Nils-Erik
INT: Heldin, Carl-Henrik
INT: ten Dijke, Peter
INTENTION: SMAD7 AND US
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SEQUENCES:
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                                                                                     Afrakhte, Mozghan
Souchelnytskyi, S
Brodin, Greger
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                                                                                                                                                                    Nakao, Atsuhito
Moren, Anita
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                                                                                                                                                      Heuchel, Rainer
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50.0%;
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al Plaza, 180 N.
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              AND USES
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              THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue

02210-2211

Boston U.S.A.

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US-08-295-060-3
, Sequence 3, Application US/08295060
; Patent No. 5659123
; GENERAL INFORMATION:
; APPLICANT: VAN RIE, Jeroen
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Best Local Similarity
Matches 123; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-MAY-CLASSIFICATION: PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      1468 ggaggggacacgcgagagcctgcgggtctatctcgcggcctctgacaagccgctgcacag 1527
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                                                                                                                                   707
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FILING DATE: 20-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-720-2441
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                                                                                                                                                  cgcacagctgctgctgggc 1726
                                                                                                                                                                                                                           gcactcgctgcgccgaaccttccccagccacatctaccgcgagaccggcaatctgcgcgc 1707
                                                                                                                                                                                                                                                                                           gtggcgcctgttcaagtcctggctcgagaaggcgcggctcgatcccagcctctacgggct 1647
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                                                                                                                                   CCAGCGGCGGCAGAAGGAC
                                                                                                                                                                                                   GCCGGCGCCACGCCGAGCGCTCGGCCCCGGAGTCCCTGAGTGCGGCGCGCGGCGAGCCC 706
                                                                                                                                                                                                                                                                   nucleic acid
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47.5%;
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                                                                                                                                US-08-464-517-5/c
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Best Local Similarity
Matches 99; Conserv
                                                                           Sequence 5, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: 26-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Fenry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1957 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                     1542
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
               APPLICANT: BEACH, DAVId H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              1662 gaaccttccccagcca 1677
                                                                                                                                                                                                                                                                                                   1602
                                                                                                                                                                                                                                                                                                                                    476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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ADDRESSEE:
                                                                                                                                                                                                                                                                                               agtectggetegagaaggegeggetegateceageetetaegggetgeaetegetgegee 1661
                                                                                                                                                                                                                                                                                                                                  CCGTGAGCAGCCGCAACCCCCACAGCCAGGGTCGCATCCGCGAGCTGTTCAGCCAGGCCG 535
                                                                                                                                                                                                                                                                                                                                                      gacagggcatccgctggtcccacacccaccttagcgagagccagctgttggcgcctgttca 1601
                                                                                                                                                                                                    TGACCACCTACGCCCA
                                                                                                                                                                                                                                                                   AGAGCCACTTCCGCAACAGCATGCCCAGCTTCGCCATCAGCGGCTACGAGGTGCTGTTCC
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P.O. Box 1404
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PERFEROEN, Marnix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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 LAHIVE & COCKFIELD
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595

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY:

USA

Boston MA

60 State

Street

02109

SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

CLASSIFICATION:

FILING DATE:

APPLICATION NUMBER: . US/08/464,517

APPLICATION NUMBER: US 07/963,308 FILING DATE: 16-OCT-1992 APPLICATION NUMBER: US 07/888,178

FILING DATE:

26-MAY-1992

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RESULT 9
US-08-463-772-5/c
; Sequence 5, Application US/08463772
; Patent No. 6066501
; GENERAL INFORMATION:
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US-08-464-517-5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          1789
                                                                                                                                                                                                                                                                                    1669
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LENGTH: 1926 base pairs
APPLICANT:
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                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                             55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Matthew P. Vincent REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 47.6 es 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      gctcgagaaggcgcggctcgatcccagcctctacgggctgcactcgctgcgccgaacctt 1668
                                                                                                                           CCAAGGCAGG
                                                                                                                                                     cgcacggagg 1798
                                                                                                                                                                                                                                                                              ccccagccacatctaccgcgagaccggcaatctgcgcgccgcacagctgctgctgggcca 1728
                                                                                                                                                                                                                                                                                                                   GAAGTAGGAGGCGCGGGGTACGTAGCGCTCCTCCAGGCCGGAGCAGGCTCTGCAGGACACG 176
                                                                                                                                                                                      ACACAGCAGCTCCATACTCGGGCAGCGAACAGGCAGGGCGGGAGTGCGGGCTCGCGAGTC 56
                                                                                                                                                                                                          tgccagcatcgagagcaccaaggagtacatcggcaacgaggcaaggccgaggccctcgatat 1788
                                                                                                                                                                                                                                                     CTGGTCCCCAGCAGCCGCGGGTCCGGGCCCGGGCCCGGGGCGCGTGCCTTCGCA 116
BEACH, David H.
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E: DNA (genomic)
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Pred. No. 0.53;
0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                            131;
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RESULT 10 PCT-US93-05000-5/c

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Best Local Similarity 47.6%;
Matches 119; Conservative
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PRIOR APPLICATION NUMBER: US 07/963,308
APPLICATION NUMBER: US 07/868,178
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: li
MOLECULE TYPE:
FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                              1729
                                                                                                                                                                                                                                                                                    1549 catccgctggtcccacacccaccttagcgagagccagctgtggcgcctgttcaagtcctg 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                175
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                           cgcacggagg 1798
                                                                 ACACAGCAGCTCCATACTCGGGCAGCGAACAGGCAGGGCGGGAGTGCGGGGCTCGCGAGTC 56
                                                                                           tgccagcatcgagagcaccaaggagtacatcggcaccgagcaagccgaggccctcgatat 1788
                                                                                                                                CTGGTCCCCCAGCAGCCGCGGGTCCGGGCCCGGGCCCGGGGGCGCGTGCCGTTCGCA
                                                                                                                                                          ccccagccacatctaccgcgagaccggcaatctgcgcgcaccagctgctgctgggcca 1728
                                                                                                                                                                                                GAAGTAGGAGGCGCGGGGTACGTAGCGCTCCTCCAGGCCGGAGCAGGCTCTGCAGGACACG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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101..940
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46
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                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                             Length 1926;
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US-08-246-361A-5/c
Sequence 5, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
APPLICANT: BEACH, David H.
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Best Local Similarity
Matches 119; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                  1609 gctcgagaaggcgcggctcgatcccagcctctacgggctgcactcgctgcgccgaacctt 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1549 catccgctggtcccacacccaccttagcgagagccagctgtggcgcctgttcaagtcctg 1608
APPLICANT: BEACH, I
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          235
                                                                                                                                                                                                                                                                                                       175
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1926 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 1993(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                             55 CCAAGGCAGG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                      tgccagcatcgagagcaccaaggagtacatcggcaccgagcaagccgaggccctcgatat 1788
                                                                                                                                                                                                                                                                                                                                                                          GAAGTAGGAGGCGCGGGTACGTAGCGCTCCTCCAGGCGGAGCAGGCTCTGCAGGACACG
                                                                                                                                                                                          cgcacggagg 1798
                                                                                                                                                                                                                                                                                                      CTGGTCCCCAGCAGCCGCGGGTCCGGCCCCGGCCCCGGGGCGCGTGCCTTCGCA 116
                                                                                                                                                                                                                               Lexington
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47.6%;
D-TYPE CYCLIN AND USES RELATED THERETO
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Pred. No. 0.53;
0; Mismatches 131;
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Best Local Similarity
Matches 119; Conserv
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CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCT-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTANTA MI REFERENCE/DOCKET NUMBER: MI TELECOMMUNICATION INFORMATION: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                     1549 catccgctggtcccaccaccctagcgagagccagctgtggcgcctgttcaagtcctg 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                    1669
                                                                                                                                                                                                                1609
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                           1789
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CITY: Boston
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                 GAAGTAGGAGGCGCGGGGTACGTAGCGCTCCTCCAGGCGGAGCAGGCTCTGCAGGACACG 176
                                                                                                                                                                                                    gctcgagaaggcgcggctcgatcccagcctctacgggctgcactcgctgcgccgaacctt 1668
                                                                                tgccagcatcgagagcaccaaggagtacatcggcaccgagcaagccgaggccctcgatat 1788
CCAAGGCAGG
                         cgcacggagg 1798
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ilarity 47.6%;
Conservative
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RESULT 12 US-08-457-245-4/c

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Best Local Similarity 45.7
Matches 138; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                           1303
                                                                                                                                                                                                                                                                                                                                               1183 gacgacacccaccaagccggcctggaacaagggccgcgttgtcgggaaaaagccgccgct 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Guy W.
REGISTRATION NUMBER: 30,617
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BARRY III, Clifton E. APPLICANT: YUAN, Ying
1483 ga 1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
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                                    397
                                                                                                                                                                                                                                                                                                                  637 GTCGATACGCCGCTCGGTGGTCAACTCCACCGACCGGCTGCACGACTACGAGCGGGTGAT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Steurre
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                         gcgcgtctcggatgtggcgaccccagctggtctgcgtgagatcgtcgagatccgccagaa 1422
                                                                                                                                                                                                                                                                             gacacctgaccagattgccctgatccgtctcatcctgcgccaggaacgggcgtggcggga 1302
                                  CGAGACGCTGTCCGACCATCACGTTCACCAACATCCATATGCCGCTGGTGGCCACCCC 338
                                                                gaagaccgaggcccgcaatgtccgccccgtacaggcccgcctgtcggaggggacacgcga 1482
                                                                                                                                                                                              tctggctctgttcaacgtggcgatcgacaccagtttgcgcggctcggacctcgtgcgcct 1362
                                                                                                      GTACAGCTCGTATCTGCCCACCAAGGCCGCGCTGGACGCGTTCGCCGACGTGGTCGCCTC 398
                                                                                                                                                                        GCGCCGGTTCGGCCACGTCGTCAACGTCTCCAGCGCCGGCGTGCAGGCCCGCAATCCCAA 458
                                                                                                                                                                                                                                              GGCGGTCAACTACTTCGGCGCGCGTGCGCATGGTGCTGGCGCGCTGCCGCATTGGCGCGA
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(415) 543-5043
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45.7%;
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Tower, One Market
                                                                                                                                                                                                                                                                                                                                                                                    Score 39.6; DB 1;
Pred. No. 0.64;
0; Mismatches 164;
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                                                                                                                                                                                                                                                                                                                                                                                        164;
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; OTHER INFORMATION:
US-08-457-245-1
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US-08-457-245-1/c
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Patent No. 5573915
                                                                                                                                 Matches
                                                                                                                                               Best
                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                               1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                      1183 gacgacacccaagccggcctggaacaagggccgcgttgtcgggaaaaaagccgccgct 1242
                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 5100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BARRY III, Clifton E. APPLICANT: YUAN, Ying
1961 GGCGGTCAACTACTTCGGCGCGCGGTGCGCATGGTGCTGGCGCTGCTGCCGCATTGGCGCGA 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                              Local Similarity
nes 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Chambers, Guy W REGISTRATION NUMBER:
                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 4158..5027
                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 521..1381
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                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 1388..2539
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Steuart Street Tower, One Market Plaza
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US-09-103-840A-2/c
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US-08-146-930-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
TILE REFERENCE: 24366-20007-00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ. ID. NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.3
Best Local Similarity 57.6
Matches 76; Conservative
                                                                                                                                     Sequence 1, Application US/08146930 Patent No. 5958764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                  3197613 CGGGTGGTCCAGGAGCTGCTCGGTCATTCCAGCCTGGCGACCACGCAGCTGTACACCCAC 3197554
                                                                                                                                                                                                                                                          3197553 GTCGCGGTCGCC 3197542
                                                                                                                       GENERAL
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APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
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                                                                                                                       INFORMATION:
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Pred. No. 48;
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NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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STREET: LOS Angeles
STATE: California
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                                                                                                                                                                                                                                                         3677 GCCGCCGCCGCCGCCGCAACTGGAGCCACCAGAGGAGCCGCCTCCGCAGCTAGA 3618
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MOLECULE TYPE:
3437
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FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 5958764 yet assigned
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: described below:
07/876,286
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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2: en,
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Match Length DB
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1 tggtgaacgcattggcttga.....tatgttgtgcaccgcgacga 8509
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19835.437 Million cell updates/sec
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  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AL066742 Drosophil
AL066051 Drosophil
AW671033 LG1_278 D
AL065629 Drosophil
BG384839 304170 MA
BG384302 303332 MA
BF078334 228572 MA
BF078334 228572 MA
BG895635 359187 MA
AW784766 115012 MA
AUT06855 Drosophil
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AW839280 CM1-LT006
AL053013 Drosophil
AL053013 Drosophil
AL054280 Drosophil
AV701967 AV701967
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10	9	10	10	10	12	10	10	12	9	10	10	10	10	10	9	10	10	9	10	10	9	12	10	10	9	12
BJ204205 BJ183869	AW497369	BF947371	BF947280	C55473	AG072425	BF194372	BM488443	AG075401	BE196050	BG365895	BG415257	BG417826	BG369006	BG369542	BE193612	BE455201	BE602055	BE194138	BG367643	BG417919	BE231844	CNS012S8	BF960900	BF962526	BE232046	вн386486
BJ204205 BJ204205 BJ183869 BJ183869	AW497369 ga59a02.y		BF947280 MR3-NN021	(n	AG072425 Pan trogl	BF194372 246388 MA	BM488443 pgm2n.pk0	AG075401 Pan trogl	BE196050 HVSMEh009	BG365895 HVSME1000	BG415257 HVSMEk000	BG417826 HVSMEk001		BG369542 HVSME1002	BE193612 HVSMEh008	BE455201 HVSMEh009	BE602055 HVSMEh010	BE194138 HVSMEh008	BG367643 HVSME1001	BG417919 HVSMEk001	BE231844 136683 MA	AL101954 Drosophil	BF960900 MR3-NN021	BF962526 PM1-NN120	BE232046 136963 MA	BH386486 AG-ND-124

ALIGNMENTS

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	FEATURES source			AUTHORS TITLE JOURNAL COMMENT	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AQ289334 LOCUS DEFINITION
/organism="Oryza sativa" /organism="Oryza sativa" /strain="Japonica" /cultivar="Nipponbare" /db_xref="taxon:4530" /clone="nbxb0034L10r" /clone_lib="CgI Rice BAC Library" /tissue_type="Leaf" /tissue_type="Leaf" /lab_host="E. coli DH10B" /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those	High quality sequence stop: 429. Location/Qualifiers 1695	TEL: 804 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: GGAAACAGCTATGACCATG Class: BAC ends	Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA	Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998) Contact: Wing RA	Oryza sativa Chrysa sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. 1 (bases 1 to 695)	AQ289334 AQ289334.1 GI:3950780 GSS. Oryza sativa.	AQ289334 695 bp DNA linear GSS 03-DEC-1998 nbxb0034L10r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0034L10r. DNA sequence.

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BASE COUNT
ORIGIN
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ACCESSION
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CM1-LT0067-280100-109-h11 LT0067 Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Bota, C., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
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seq primer: puc 18 forward  
High quality sequence start: 37  
High quality sequence stop: 442.
- Web; www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute by partial NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                             prosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
Nuscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BACR19D16 of RPCI-98 library from
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acccaccttagcgagagccagctgtggcgcctgttcaagtcctggctcgagaaggcgcgg 1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STSKSSSGSSSSSSYTTSKSTSASGSGSWSAGGGSGSTGSTSSSSSSSTSTSSSSV 711
• Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further informat
                                                                                                                                                                     Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Www.ronarcha; Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome sur
BACR19D16 of RPCI-98 library from
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                                                                                          Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                 Direct Submission
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/db_xref="taxon:7227"
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/clone="BACR19D16"
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/note="end : 51 g 172 t 511
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segref@genoscope.cns
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REFERENCE

Muscomorpha;

comorpha; Ephydroidea; (bases 1 to 839)

TITLE

Genoscope.
Direct Submission

Submitted (02-JUN-1999)

Genoscope -

Centre National de Sequencage

AUTHORS JOURNAL

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RESULT
CNS004NB
                                                                                     SOURCE
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                                                                                                                              VERSION
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                       Drosophila Eukaryota; Pterygota;
                                                                                                                                                                   CNS004NB
Drosophila melanogaster genome sur macR10E16 of RPCI-98 library from seguence.
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/db_xref="taxon:7227"
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Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
a; Ephydroidea; Drosophilidae; Drosophila.
                                                                  melanogaster
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCl-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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AV701967 ADB Homo sapiens
AV701967
AV701967.1 GI:10718297
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                                                                      Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 421)
Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
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/db_xref="taxon:7227"
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67 c 77 q
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Pred. No. 0.1;
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Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 1 201203, P. R. China Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                  CNS0072Q 1932 bp DNA linear GSS 03-JUN-1
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE [E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) Betermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                  Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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This clone is available at C
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            fly), genomic AL066742
                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                               fruit fly.
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/clone_lib="ADB"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                   Lrutt 11.
Drosophila melanogaster
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Etarygota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACR14809"
/note="end : T7"
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                                                                                                                                                                                                                                                                                                                           gagcaagccgaggccctcgatatcgcacggaggtatcacctctaacccatggagac 1821
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Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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LG1_278_D03.b1_A002 Light
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                                                               sorghum
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/clone_lib="RPCI-98"
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Best Local Similarity
Matches 175; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGAGACACTCGCCGGCGTGAACCCCCTGATCATCAGGCGTCTGACGGAGTTTCCTCCGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46
                                                                                                                                                                                                                                                                                        cgcggctcgatcccagcctctacgggct 1647
                                                                                                                                                                                                                                                                                                                                                                                                      cccacacccttagcgagagccagctgttgggcgctgttcaagtcctggctcgagaagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGGACCACCACGACCACTACATGCCGTTCCTGATCGAGGTCAACAGCCTGGACGACA 345
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2 (bases 1 to
Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL065629
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Lilic clade; Panicoideae; Andropogoneae;
                                                                                                                CNS006ON
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/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Ecol
: The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 181 c 157 g 70 t
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                                                                                   linear GSS 03-JUN-1999
ence T7 end of BAC #
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VERSION
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ORGANISM
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                                                        1703 cgcgccgcac 1712
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488 CDCCCCCCCC
                                                                                                                 548 CCSCSCACCRCCCCCRSCSCGCCCMSSSCCSSCCCCCCCASMCCAWAMAHACCCSCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggctgcactcgctgcgccgaaccttccccagccacatctaccgcgagaccggcaatctg 1702
                                                                                                                                                                                                                                                                                                                                                   ASAAASARSASRASAVMAVAVAASSSAVASSGSSSVSCSSSRCGCSASSSSASASSGSSS 609
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Eukaryota; Metazoa; Artropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 910)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL065629.1
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/clone_lib="reclips"
/clone="back14121"
/clone="back14121"
/note="sac 177"
a 63 c 112 g 1
   479
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15.7%; Pred. No. 0.71;
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Best Local Sim
Matches 161;
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                          tcggcaccgagcaagccgaggccctcgatatcgcacggaggtatcacctcta 1809
                                                                                                                                            TGTTCCGGGAGCCGGCCACCATCAACTACCCATTTGAGAAGGGCCCGCTGAGCCCGCGCT
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                                                            AGCTTTGCGAGGCCGTCTGCCCTGCCCAGGCCATCACCATCGAGGCCGAGCCGAGGGCCG
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304170 MARC
BG384839
BG384839.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 93 row: F column: 1
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 402 762 4366
Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SFURIO; JIC, /note="Vector: pCMV SFURIO; JIC, Library made from pooled tissue and 30 embryos."

a 174 c 155 g 75 t
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Eutheria; Cetartiodactyla; Suina; Suidae;
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Sus scrofa (
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                                                                                                                                                                                                                                                                                                                                                                                 Score 46.4; DB 10;
Pred. No. 0.64;
0; Mismatches 191;
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rom pooled tissue from day :
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  day 11, 13, 3
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Best Local S
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                                                                                                                              totacgggctgcactcgctgcgccgaaccttccccagccacatctaccgcgagaccggca
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                                                AGCTTTGCGAGGCCGTCTGCCCTGCCCAGGCCATCACCATCGAGGCCGAGCCGAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                     161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
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303332 MARC 1PIG Sus scrofa
BG384302
BG384302.1 GI:13308774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: J column: 21
Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                   h 0.5%;
Similarity 45.7%;
61; Conservative
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/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
180 c 158 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
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                                                                                                                                                                                                                                                                                                                                                                   ; Score 46.4; Di
; Pred. No. 0.65
0; Mismatches
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res 161; Conserv
               atotgogogogoacagotgotgggooatgocagoatogagagoaccaaggagtaca 1757
 AGCTTTGCGAGGCCGTCTGCCCTGCCCAGGCCATCACCATCGAGGCCGAGCCGAGGGCCG 447
                                                                             CAGCCCAGACCCTGCTGTGGACCGAGCTTGTCCGAGGCCTGGGCATGACCCTGAGCTACT
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PO Box 166 Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass Sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF078334
228572 MARC 2PIG Sus sc
BF078334
BF078334.1 GI:10872101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 50 row: J column: 9
Seq primer: ATTTAGGTGACGATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegrand Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Design and use of two pooled tissue normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGANACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            karyota; Metazoa; Chordata; Craniata; Vertebrata;
mmalia; Eutheria; Cetartiodactyla; Suina; Suidae;
(bases 1 to 512)
                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 183 c 164 g 74 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                            0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512
s scrofa c
                                                                                                                                                                                                                                                                                                            Score 46.4; DB 10;
Pred. No. 0.65;
0; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 bp
cDNA
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4 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
sequence
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA libraries for
                                                                                                                                                                                                                                                                                                                                             512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 18-OCT-2000
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Casas, E.,
                                                                                             1697
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                                                               387
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RESULT 14
BG895635
LOCUS
DEFINITION
ACCESSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
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ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                    Matches
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                    1698
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atotgogogocogoacagotgotgogocatgocagoatogagagoaccaaggagtaca 1757
                                                                                                                                                            agagccagctgtggcgcctgttcaagtcctggctcgagaaggcgcggctcgatcccagcc 1637
                                                                                                                                                                                                                                                                                                      cccgcctgtcggaggggacacgcgagagcctgcgggtctatctcgcgggcctctgacaagc 1517
                                                                           totacgggctgcactcgctgcgccgaaccttccccagccacatctaccgcgagaccggca 1697
                                                                                                                                                                                                        CAGCCCAGACCCTGCTGTGGACCGAGCTTGTCCGAGGCCTGGGCATGACCCTGAGCTACT
                                                                                                                                                                                                                             ACGGCAGCCGCCGCGCGCTATGACATCGACATGACCAAGTGCATCTA
                                                        TCCGCGGGGAGCACGCCTGCGCCGGTACCCATCCGGGGAGGAGCGTTGCATCGCCTGCA
                                                                                                                               TGTTCCGGGAGCCGGCCACCATCAACTACCCATTTGAGAAGGGCCCGCTGAGCCCGCGCT 314
                                                                                                                                                                                                                                                                                                                                                      161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 544)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG895635 544 bp mRNA linear 359187 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG895635 GI:14305876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
v0.980904.e. Vector identified by cro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166,

Tel: 402 762 4366

Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normalized EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 123 row: D column: 8
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRIMETS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                                                                                                                                                                    0.5%;
Similarity 45.7%;
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="0H108"
/note="Vector: pcMV SPORT6; Site_Library made from pooled tissue find 30 embryos."
a 194 c 172 g 81 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Score 46.4; DB Pred. No. 0.68; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 led and alt_trimmed with phred
cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                      191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site_1: xbaI; Site_2: xhoI;
ssue from day 11, 13, 15, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith, T.P.L.,
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                                                                                                                                                                                                                                                                                                                                                        0;
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                                                            374
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1758 tcggcaccgagcaagccgaggccctcgatatcgcaccgaggtatcacctcta 1809

375 AGCTTTGCGAGGCCGTCTGCCCTGCCCAGGCCATCACCATCGAGGCCGAGCCGAGGGCCG

434

435 ACGGCAGCCGCCGGACCACGCGCTATGACATCGACATGACCAAGTGCATCTA 486

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RESULT 1
AW784766
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ORIGIN
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                       Query Match 0.5%;
Best Local Similarity 45.7%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                1578
                                                                                                                                                                          1458 cccgcctgtcggaggggacacgcgagagcctgcggggtctatctcgcgggctctgacaagc 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                   127
                                                                                                                                                    187 CAGCCCAGACCCTGCTGTGGACCGAGCTTGTCCGAGGCCTGGGCATGACCCTGAGCTACT
   307
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                                                                                                 tctacgggctgcactcgctgcgccgaaccttccccagccacatctaccgcgagaccggca 1697
                                                                           TGTTCCGGGAGCCGGCCACCATCAACTACCCATTTGAGAAGGGCCCGCTGAGCCCGCGCT
                                                                                                                                                                                                                             TCCGCGGGGAGCACGCGCTGCGCCGGTACCCATCCGGGGAGGAGCGTTGCATCGCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 558)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreld, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW784766 558 bp mrNA linear 115012 MARC 1PIG Sus scrofa cDNA 5', mrNA sequence. AW784766 AW784766.1 GI:7841542 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 43 row: M column: 13 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
/ob_xref="taxon:9823"
/clone_lib="Marc lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Ilbrary made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
a 200 c 175 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                     Score 46.4; DB 9; Length 5
Pred. No. 0.69;
0; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                          Length 558;
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                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                      246
                                                                           306
                                                                                                                                                                                                                                                                                                         0;
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Search completed: August 20, 2002, 09:12:11 Job time: 10889 sec

В

427

ACGGCAGCCGCCGGACCACGCGCTATGACATCGACATGACCAAGTGCATCTA 478

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             GenEmbl:*

1: gb_ba:*
2: gb_htg:
3: gb_ln:*
4: gb_om:
5: gb_pt.
6: gb_pt.
6: gb_pt.
9: gb_pr.
10: gb_r.
11: gb_s.
12: gb_s.
12: gb_s.
12: gb_s.
13: gb_l.
14: gb_l.
15: em_l.
16: em_l.
17: em_l.
18: em_l.
20: em_l.
21: er.
22: er.
23: er.
23: er.
24: er.
25: e.
26: e.
27: {
28: ...
31: ...
31: ...
33: ...
 Score
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Query
Match Length DB
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2517
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1797656 segs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         August 20, 2002, 19:01:33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version
Copyright (c) 1993 - 2000
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gb_htg:*
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 IJ
                            SUMMARIES
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Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3595312
Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2517
                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                          DEFINITION
ACCESSION
VERSION
                                                                                                                                                                            RESULT
AX281576
                                                                                                                                                                    LOCUS
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ALIGNMENTS

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ACCESSION
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KEYWORDS
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AX281576.1 GI:16608828

**EFFERENCE | (sites)
AUTHORS | D'Elia, J.

TITLE
JOURNAL | Patent: WO 0177347 - A 18-OCT-2001;
FEATURES
SOURCE | Location/Qualifiers
Source | Journal | John (US)
FEATURES | Location/Qualifiers | John (US)
FEATURES | J. 2517
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PAT 02-NOV-2001

synthetic construct.
synthetic construct
artificial sequence.

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D'Elia,J.
Ketogulonigenium shuttle vectors
Patent: WO 0177347-A 1 18-OCT-2001;
Archer-Daniels-Midland Company (US); D'Elia, John (US)

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Archer-Daniels-Midland Company (US)
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Sequence 1 from Patent W09940220.
AX019311 GI:10043298
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Patent: WO 9940220-A 1 12-AUG-1999;
GAUTHIER JEAN MICHEL (FR); GLAXO GROUP
Location/Qualifiers
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57; Conserv
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Homo sapiens junctophilin
AF429315
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 125020) 1 (bases 1 to 125020) 1 (bases 1, Callahan, C., Rosenblatt, A., Callahan, C.,
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                                                                                                                        WYYVKYBSMSVSARKSKGHKVRBSSMKCSRRKDMSTSSMWRSMKDRKCSRCSHSHYSKSM
                                          GKWTSDVDRCYACSSBMKYKMHRKKHYKKDSHBSWGKSHMKKGAWRVRSMYRSMRCSVHD
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/note="isolated from a patient with Huntington Disease-Like 2 (HDL2)"
complement(35581. .35746)
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/gene="JPH3"
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/db_xref="taxon:9606"
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/product="junctophilin 3"
/protekin_id="AAL40941.1"
/protekin_id="AAL40941.1"
/db_xref="GI:17646245"
/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWSHGFEVLGYYTRPSGNTYQGTWAAQGKKHGIGLESKGKWVYKGEWTHGFKGRYGVRECAGNGAKYECTWSNGLQDGYGTETYSDG"
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/gene="JPH3"
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                                                                                           CCAACCGCCGAGTCCCACCACGAAGAGCCTGAGCTCCTG
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Sequence
AX024269
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Patent: DE 19846493-A 13-APR-2000;
BIOTECHOLOG FORSCHUNG GMBH (DE)
Location/Qualifiers
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/db_xref="taxon:56"
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aaagcggtaaaatttccggtaaaaaagatgaatctggggcatgggttatagatcctgcag 1713

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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ORGANISM
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Best Local Similarity 50.7%;
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actgcgggcggccgcatggctgatgatgtgcgccatgaaatgcggctggccgacattcgc
                                                                                                                                                                                                                                                                                Sequence
166494
                                                                                                                                                                   1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beyer S. and Mueller R.J.
Patent: DE 19846493-A 74 13-APR-2000;
BIOTECHNOLOG FORSCHUNG GMBH (DE)
Location/Qualifiers
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Polyangium cellulosum
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/db_xref="taxon:56"
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (06-APR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C.elegans Sequencing Consortium 2 (bases 1 to 32784) Steward, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 282 (5396), 99069613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; Collagen; Transfer RNA; tRNA-Arg; UDP-glucuronosyltransferase like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270682
                                                                                                                                                                                                                                                                                                                               available incommended.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone F08G5. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   none
                                                                                                                                                        sequence Z70680.

The true left end of clone C25G4 is at 32680 in this sequence. The true right end of clone F28D1 is at 725 in this sequence. The start of this sequence (1. .103) overlaps with the end of sequence Z70684 The end of this sequence (32680. .32784) overlaps with the start of
                                                                                                                                                                                                                                                                neighbouring submissions. The true left end of clone F08G5 is at 1 in this sequence. The true right end of clone F08G5 is at 7448 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available information.
the specified clone. It may be shorter to overlapping sections once, or longer becoverlap between neighbouring submissions
                                                                                               For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                            [MPORTANT:
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                 ence is NOT necessarily the entire insert of It may be shorter because we only sequence once, or longer because we arrange for a small
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/gene="F08G5.1"
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                                                                                                                                                                                                                       preliminary prediction similar to tRNA-Gln"
                                                                                                                                                                                                                                                                                                                               complement(10702.
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join(4263...4329,4376...4555,4855...5113,5309...5738,
5788...5943)
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complement(join(6848. .6998,7613.
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8357. .8473))
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predicted using tRNAscan-SE-1.11
preliminary prediction
similar to tRNA-Gln"
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27016...27170,27239...27395,27512...27936,27983...28079,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join(23649. .23704,23750. .23840,24635. .25069,25364. .2
25854. .26015,26074. .26241,26402. .26465,26511. .26554,
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28542. .28762)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(21306. .22064,22117.
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/gene="F08G5.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar to tRNA-Arg"
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/gene="F08G5.t1"
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.30308,30695. .31054,31781. .319
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                                                                                          .31951)
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
AF429315.1 GI:17646244
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Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwans, Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, I Potter, N.T., Ross, C.A. and Margolis, R.L.
Potter expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

associated with Huntington disease-like 2

Nat Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers
1. .125020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmes, S.E., Inger
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
complement(35581. .35746)
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/db_xref="GI:3875595"
/db_xref="SPTREMBL:Q19223"
                                                                                                                                                                                   /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                      NGAKYEGTWSNGLQDGYGTETYSDG"
                                          /translation="mSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
                                                                                    /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                                                                                                                                                                                         complement(<36507. .36887)
                                                                                                                                                                                                                                                                                  /note="JP3"
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/db_xref="taxon:9606"
/chromosome="16"
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                                                                                                                                                                                                                                   /gene="JPH3"
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4254 others
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                                                                                                                                                                                                                                                                                                                                 YSTKSYKSGRRKSKGWGRSTKSKAKSSMRMAGSKCTYGSSYWSNNRRNNRMGKTGCNYMY
                                                                                                                                                                                                                                                                                                                                               AGRGCYSSSMWSTRKRRSKCYSYKKSYKKGRGKMKGWGGMKRGSKYWSSMKKMKRSSWSKC
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                                                                                                                                                                                              KMKMYKSYYRRKRWNTCMKMCYSMYMAMYCRSMCCNCMCKSCCGCYSMGMSSYSYSGKYS
                                                                                                                                                                                                           SGTRRRCMKSKCRRGSRGKSMGMTRGRSGGKTSYSAKGSGRGCYYCWGWGRKGRKCMSSR
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                                                                                                      STRGSSAGKKSSYKKMSCCARYKSMS
                                                                                                                    agacgacccaaccgtcgccaggcgcg;;;;;;;!||
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BOS taurus mRNA for IkB
AJ414556
AJ414556.1 GI:15986410
bIKKbeta gene; IkB kinas
                                               BTA414556
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Rottenberg, S., Dobbelaere, D.A.E. and Heussler, V.T. Identification and characterisation of the bovine (IKKS) alpha, beta and gamma
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Institut fuer Tierpathologie/Uni Bern,
Bern, SWITZERLAND
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                                                                            GCTGCCCAAGCTGGAGGAGGTGGTCAGCCTGATGAGCGAGGACGAGAAGATGGTGGTGCG
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36. .2306
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-OCT-1999) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicir Baylor Plaza, Houston, TX 77030, USA On Sep 24, 1999 this sequence version replaced gi:5739555 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                        CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 204917)
of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
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Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
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Genes and Region of sequence similarity are

identified by BLAST

(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation html.

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16816. .16837
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AL048825, AA278956, and W38986"
complement(14286. _14586)
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13556.
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/chromosome="3q26.2-27"
/clone="RPCI11-379K17"
766. .1132
                                                                                                                                                                                                                                                   complement(17196. .1
/rpt_family="MER112"
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/rpt_family="MER46A"
                                                                                                                                                                    AI522162
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18072. .19357
                                                                                                                                                                                                                                                                                                                                                                                     /note="Region: Unigene cluster containing AI042019 and
AI890489"
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15264. .15890
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/db_xref="dbSTS:55264"
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1. .204917
                                               /rpt_family="AluJo"
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AI522162, W31729 and AA354506"
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complement(24639...24744)
/rpt_family="HERVK22"
complement(24750...25603)
/rpt_family="HERVK22"
complement(25606...26058)
/rpt_family="LTR22A"
/rpt_family="LTR22A"
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/rpt_family="Charlielb"
complement(26391. .26559)
/rpt_family="MIR"
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22470. .22760
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28982. .:
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27836. .28013
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28688
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complement(31674. .31950\
/rpt_family="MSTB"
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/rpt_family="MSTB"
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complement(31595. .316
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Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Riesen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Eisen, J., Heidelberg, J.F., Ralley, M.R.K., Ohta, N., Maddock, N.D., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vanathevan, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Venter, J.C., Shapiro, L. and Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and Fraser, C.M.
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Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21173698
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/note="identified by
PF00675"
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79. .3009
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                                                                                                                   EYWVGALSGAHTDPRLLDATRSVIAGLSRVTPADVQKAAQTYLADEKSWLLLVKPEAA
                 complement(3071.
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3970. .4722
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VGAGSTAGGVVNYYGGGGHGGYYSGPMATGYIQGLNSRRQAYEARTTSTRRV
IVRAVCLDDRAVPHAASQVTPDREIDBAYDGELYRCIAGARLQYVIAPTGGHIDISTG
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LVEAGRQAGHKTTKDFNGYQOEGFGFYDLTINDGQRWSAAMAYLNQALSRPNLTCVTE
ACTTRIILDKRRAVGVEYVVGKSREKQVAYADAEVLLSAGAVQSPQILQLSGIGAAED
LAPHGIAVAHESKGYGANLODHLDVCYSWTAKNLKTYYSANKGLNKLGVGMNYMFFGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5674..7341)
/gene="CC2642"
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/gene="CC2641"
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spwpgspskpravensrartrogttmftpsterlidymrakkgqaalprradidpgef
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                                                                                                                                                                              GLGRQQFLESGAFLKSRPDLDRPDLQIHGVLAIMQDHGKVVVEKDGFTLHVCQLRPES
RGKVGLRSADPFDDPTILGNYLATEEDRRAIREGVRIARETVAQAAFDPYRDAEYAPG
                                                                                                                                                                                                                                                                                                                                                                                                                    /product="choline dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00732"
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LKASLDVSTASGLARY ET IQPKFNLVDRDQVEGALAELANAEGLG I I PYYGLAAGFLT
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/db_xref="GI:13424220"
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RKRRTPVVVTADIRAHGVPSVGMEVLFAPLQGASGETDRFLGLYQPIAMTARLMGRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
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                                                                                                                          MPTLIGGNTNAPTIMIAERAADLIRGKTPAAPLDVPVYEDGRAVAAE"
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                                                                       /gene="CC2643"
                                                                                                                                                         <u>ADVKSDADLDAWIRSKAETIYHPVGTCRMGVAGDPMAVVDDQLRVQGVQGLRVIDASV</u>
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  11468 TGCGCAAGACCAGCCACGAGCCTCAGCCTGCCGCCGCTGGGCCTGGGCCTGGCGATCT 11527
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                           707 acggcatgaaaaaccatgaccgtgagagcctgaccccgctgttcgaggagctagccgctg 766
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Local Similarity
                            gcggccgcatggctgatgtgcgccatgaaatgcggctggccgacattcgcgcaatcg 706
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PID:1651507; ide
                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="oligopeptide transporter, OPT family"
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9453. .9758
                                                                                                                                                                                                                                             AKGYLGGNLDWGLLGYGALIGLGLVAVDAILRKTSHERLSLPPLGVGLAIYLPSSVTAPVVVGALAGWLYEKVVSKDRAAEPSRRLGVLIASGFIVGESLFNVSLALLIVSTGKGDPLALPFAPSEHVGMFLSLAAAAIVVVGFYRWARKAGAKAMEA"
                                                                                                                                                                                                                                                                                                                             AAIWTLAKLVGPITSGLKSAFAAAQARKAGGAKLPRVEQDIPIGIVGLVSVLLLAPAG
WELAHFLTGGPLASLTTPLVAIGIGYLVFAGLLAAAVCGYMAGLIGSSNSPVSGIAIL
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9853. .11853
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8525. .9277
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/transl_table=11
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/transl_table=11
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                                                                                                                                   Score 42.8;
Pred. No. 3;
                                                                                                            Mismatches
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AAS18309 12-MAR-2002 (first entry) AAS18309; AAS18309 standard; DNA; 2517 BP

DNA region of Ketogulonigenium plasmid pADM291 supporting replication.

Cloning vector; Ketogulonigenium replicon; endogenous plasmid; pADM291; transformed host cell; Escherichia coli; plasmid vector replication; ds

Ketogulonigenium sp. strain ADM291-19

WO200177347-A2

18-OCT-2001.

05-APR-2001; 2001WO-US11059

05-APR-2000; 2000US-194625P

(ARCH) ARCHER-DANIELS MIDLAND CO. (DELI/) D'ELIA J.

D'Elia J;

WPI; 2002-049150/06

Human immune syste

Novel nucleic acid vector comprising Ketogulonigenium replicon a specific deposited endogenous plasmid, useful for producing found on

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Ketogulonigenium endogenous replicon; plasmid pADM291. plasmid;

Ketogulonigenium sp. strain ADM291-19 coli; pADM291; circ circular; cyclic;

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05-APR-2000; 05-APR-2001; ARCHER-DANIELS MIDLAND D'ELIA J. 2000US-194625P 2001WO-US11059

18-OCT-2001

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The present invention relates to the isolation of vectors comprising a Ketogulonigenium replicon found on the endogenous plasmid, pADM291. The invention also describes methods of transforming host cells with the vectors and producing polypeptides and/or antisense transcripts by culturing the transformed host cells. The vectors are useful for transforming a host cell by conjugation or electroporation. The vectors which have a replicon functional in both Ketogulonigenium and Escherichia coli, enable the cloning of certain genes of Ketogulonigenium in E.coli as the latter is an efficient host for amplification of vector DNA. The present DNA sequence represents the replicon of Ketogulonigenium endogenous plasmid pADM291.
                                                                                                                                                                                                                                                                                                       Novel nucleic acid vector comprising Ketogulonigenium replicon found a specific deposited endogenous plasmid, useful for producing polypeptides and/or transcripts by culturing host cells transformed with vector
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a specific de polypeptides with vector

nucleic acid vector comprising Ketogulonigenium replicon cific deposited endogenous plasmid, useful for producing eptides and/or transcripts by culturing host cells transf

transformed

9

Novel

Claim

3

Fig

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English.

D'Elia

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2002-049150/06

The present invention relates to the isolation of vectors con a Ketogulonigenium replicon found on the endogenous plasmid, the invention also describes methods of transforming host cet the vectors and producing polypeptides and/or antisense transculturing the transformed host cells. The vectors are useful transforming a host cell by conjugation or electroporation.

transcripts seful for

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Antisense; ds; prokaryotic cellular proliferation gene,
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                                                                                                                                                                                             DNA;
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49.5%;
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26-MAY-2000;
23-OCT-2000;
                                                                                                                                  1703
                                                                                                                                                                                                                                                                                                                          The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
1823 aaagccagtaccgttaccagaccaccaatccgaaaatcttcg
                                                                 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; Seq ID No 6149; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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Yamamoto RT,
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22-DEC-2000;
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                                                                                                                                                                                                                                                                              Sequence 1980 BP; 452 A; 518 C; 585 G; 425 T; 0 other;
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                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                                 809
                                                                                                                                             548 aaactgtgctccctgccgaggtggcgagaggggtctatatgcgcaatccgccccgcctgc
                                                                                                                                                                                                                Local Similarity
                                                                                aggogotcaagotcatgcatttaatgatagocaactgogggoggcogcatggotgatgatg 667
                                                               cgtggctggagtcgcacggtgtaacggtagacaaatggggccgcatcatcgcggatgtgg
                                                                                                                              aatttgtcatgccagccgacgcggtgattatggcgtttggcttcaatccgcacgggatgc
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                  tgcgccatgaaatgcggctggccgacattcgcgcaatcgacg
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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ВP

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В
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CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO at figure in the printed content of the invention.
   Вb
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Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder;
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 1688 cgtggctggagtcgcacggtgtaacggtagacaaatggggccgcatcatcgcggatgtgg 1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 17600; 103pp; English
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                                                                                                                         Local Similarity
mes 86; Conser
                 aatttgtcatgccagccgacgcggtgattatggcgtttggcttcaatccgcacgggatgc
                                                                             2001-639362/73
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2000US-0649167.
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393

acgaaaattacacataattatcaatagcttattcgcttaaaagggagtaattgggccgca 390

8757

CCTACTATTACCAATAAATTTCACTAAAATATTCCATAAAACGTTATTTAATATAACTCA 8697

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RESULT 9
ABL34134/o
ID ABL341
AC ABL
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                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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01-SEP-2000;
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                                                                                                                                                                                                                                          Sequence 10886 BP; 3239 A; 130 C; 2418 G; 5099 T; 0 other,
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actttttcacaatcaaaaaatgggcgaagcccttcttgttctatagttcttatagttcat 330
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                                                                                                                     Similarity
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2000DE-1043826
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Pred. No. 1
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AAH24065;

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RESULT ABL34011 ID ABL34011 ID ABL34011 ID ABL34011 ABL ACC ABL XX ABL X
RESULT 11
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ID AAH240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADIS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
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01-SEP-2000;
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antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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     AAH24065 standard;
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2000DE-1043826
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psoriasis; bowel disease;
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hormone-sensitive lipase stimulation;
carboxylase inhibition; obesity;
fat/lean ratio; food use; ds.
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05-NOV-1999;

99AU-0003875

(META-) METABOLIC PHARM LTD

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The invention relates to novel transgenic organisms useful in the cc production of functional food and drink products for the treatment cc prevention of obesity via the regulation of lipid metabolism. The corganisms comprise a polynucleotide encoding a growth hormone fragment cc enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key cc enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key cnyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key crown the full-length growth hormone fragment preferably contains cc enzyme in lipogenesis). The growth hormone gragment preferably contains cc entree the full-length growth hormone) and is optionally linked to an cc cont the full-length growth hormone) and is optionally linked to an cc epitope tag or heterologous fusion protein partner. The transgenic cc erganism may be a microorganism used to produce a fermented product organism may be a microorganism used to produce a fermented product cc eig., yeast), or an edible plant or animal or cell thereof. Food or cc eig., and may also be used to treat or prevent obesity, particularly cr in humans, and may also be used to improve the fat/lean ration of livestock raised for meat production. In the exemplification of the convention, the human growth hormone (hGH) fragment analogue AD9604 was in present sequence is described as a DNA sequence from yeast in the sequence listing, but is not further referred to in the
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les 38; Conserv
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                                                                                                                                                                                                                                                                                                                              catttctccccatgggaaagacaacacaagtggccgcagaccgggccttcgaccagacaa
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RKKHKAGHMSRHNWKDSVKATKY
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                             gtgagagcctgaccccgctgttc 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4590;
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                                                                                                                                                                                                                                                                                                                                                                                     4083
                                                                                                                                                                                                   667
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                                                                                                                                                                                                                                                                          607
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RESULT 12 AAS87283/c ID AAS87283

standard; cDNA; 2047

ВP

0;

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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II) the CC constraints of the const
                                QΥ
                                                                           В
                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 23087; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABG23096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                             1016
                                                                                                                                                                                                                                                             Sequence 2047 BP;
                                                                                                     369 aaaagggagtaattgggccgcaaaagggagtaattgggccgcaaaagggagtaattgggc 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73
                     cgcaaaagggagtaattgggccg 451
                                                                             ACACAGGAGTATTGGGGATGCACACAGGAGTATTGGGGGATGCACATAGGAGCACTGGGGA 957
TGCACATAGGAGTATTGGGGACG
                                                                                                                                                                 55,
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0540217.
2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                  402
                                                                                                                                                                                      1.5%;
                                                                                                                                                                                                                                                               A; 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic protein #23087
                                                                                                                                                                     0;
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                                                                                                                                                                                           Pred.
                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                        589
                                                                                                                                                                       Mismatches
                                                                                                                                                                                        38.2;
No. 1.
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5
                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                        T; 0 other
                                                                                                                                                                                                                23;
                                                                                                                                                                         28;
                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      torensic;
                                                                                                                                                                                                                    2047;
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                                                                                                                                                                                                                                                                                           RESULT 13
AAI61373/c
ID AAI61373 standard;
밁
                                                                                                           Db 410772
                                                                                                                                                               Db 410832 TAACAATATGCATTGAGAAGGTAATTATCATAATATATAATAAATTTGCTAAAAATCAAG
                                                                                                                                                                                                                     Query Match
Best Local·S
Matches 105
 410652
                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                          2184
                                                                               2124
                                                                                                                                     2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyst
                                                                                                                                                                                        2004 ttaaaacctgaatcagcattctagcgatgctgataagaagtaaatatagccacaatagag
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                     these proteins. The present sequence is a nucleic acid molecule provided in the specification.
                                                                                                                                                                                                                                                                                                                                                 nucleic acid molecules, as well as antibodies capable of recognising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 30; Page 596-893; 1353pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hauge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MONS ) MONSANTO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JAN-2000; 2000US-0174880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-2001; 2001WO-US00552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
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                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified nucleic acid for t nematode resistance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bean; antihelmintic; gene therapy; soybean cyst nematode; SCN;
resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
pl7 region G3; 318013 region A3; 515002 region G2; ds.
                                                                                                                          cggccattttccattcacatacagctcatcatgtgatcaatatcaagtattgatattcat 2123
                        agtgctaacataactatcgctggccctaaagaagatt 2220
                                                                           caatggagaagaatttacatgtatcacaggatcatcacagcatttgtttttgtatttcta
                                                                                                           2001-425872/45
AATTCAATGTTGCCTATATATAACTCCAAAAAATGTT
                                                     ATATGATTACATAGAAATTAAACTCATTGAATCATCTCATTAGTTATTTTTATTTTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM,
                                                                                                                                                                                                                        105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         max.
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                                                                                                                                                                                                                                                                                           513445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang ML,
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                         BP; 173367 A; 85402 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                  1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parsons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513445
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                     Score 37.8; D
Pred. No. 61;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parnell LD;
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                                                                                                                                                                                                                                                                                           83912 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a soybean plant having plant breeding programs
                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                       112;
                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                           170492 T;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                  513445;
                                                                                                                                                                                                                                                                                           272 other;
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soybean
                                                                                                                                                                                                                     Gaps
                                                                               2183
                                                     410653
                                                                                                                                                                 410773
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AAF26561/c
ID AAF265
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy - \frac{1}{2}
                                                                                                                                                   2762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins may be used in the prevention, diagnosis and treatment diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2000; 2000WO-US15137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF26561 standard;
2642
                                   2183
                                                                         2702
                                                                                                               2123
                                                                                                                                                                                         2063
                                                                                                                                                                                                                               2822
                                                                                                                                                                                                                                                 2003 tttaaaacctgaatcagcattctagcgatgctgataagaagtaaatatagccacaataga
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to 26 secreted human proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 449-454; 525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071148/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                               aagtgcta 2190
                                                                                                                                                                           gcggccattttccattcacatacagctcatcatgtgatcaatatcaagtattgatattca
GAAAACTA
                                                                                                                                                                                                                             TACTTAGCAATGATTATATTTATAAGATATCCATATAAAAGATCTTTGTTCTTTTAAT
                                                                                                           tcaatggagaagaatttacatgtatcacaggatcatcacagcatttgtttttgtatttct
                                                                                                                                                 TCATCAAAATATTACTCAATTGTCTGCCAGGATTGTTGCGATAGCAACAACTTAACTTCT
                                                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          abnormal angiogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases.
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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. 2635
                                                                                                                                                                                                                                                                                                                                                                                                    BP; 1329
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                                                                                                                                                                                                                                                                                                                      1.5%;
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                                                                                                                                                                                                                                                                                                                      Score 37.6;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #15
                                                                                                                                                                                                                                                                                                                                                                                                    <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                    1324 T;
                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                    \vdash
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation
                                                                                                                                                                                                                                                                                                                                            4043;
                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                           2182
                                                                                                                                                 2703
                                                                                                                                                                                                                                                                 2062
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RESULT 15 AAF64182/c ID AAF64182 standard; cDNA; 4044

Qγ Db Qγ В

0

밁 ρy Вp

AAF64182

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Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide CC sequences AAF64176 - AAF64224. The specification includes amino acid CC sequences AAB75555 - AAB75606 which represent fragments of the human CC secreted proteins, and protein sequences with which they share homology. CC The proteins and polynucleotides, their agonists and antagonists have activities dependent on the tissues and cells in which they are care expressed, examples of these activities include, immunosuppressive; CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; CC virucide; fungicide, opthalmalogical; and vulnerary. The proteins, cc polynucleotides, agonists and antagonists can be used to treat or disgose various diseases and disorders including, autoimmune cc e.g. cardiac arrest, cerebrovascular disorders including, autoimmune cc e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, cc angiogenesis, neurous system disorders e.g. Alzheimer's disease, cc angiogenesis, neurous system disorders e.g. Alzheimer's disease, cardiavascular disorders e.g. cerebral ischaemia, cc e.g. corneal infection. The polypeptides can also be used to aid wound continue and poithelial cell proliferation, to prevent skin ageing due to content of primary tissues, to regenerate tissues and in chemotaxis. The colynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which care used in the isolation, identification and characterisation of the proteins of the invention.
Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic, neuroprotective; antipacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; cardiovascular disorder; hyperproliferative disorders; cerebrovascular disorder; wound healing; nervous system disorder; ocular disorder; skin ageing; chemotaxis; food additive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 439-440; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071258/08
P-PSDB; AAB75512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2000; 2000WO-US14973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein gene 7 SEQ ID NO:17.
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                                                                                                   Sequence 4044 BP; 1329 A; 695 C; 695 G; 1323 T; 2 other
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1.5%;
milarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsoulis GA;
Score 37.6; DI Pred. No. 3.4; 0; Mismatches
                                      DB
                                      22;
                                      Length 4044;
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94;

Indels

0;

Gaps

0;

100

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Search completed: August 20, 2002, 21:33:26 Job time: 5893 sec

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ALIGNMENTS

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Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/07/935,313
FRIOR APPLICATION DATA:
APPLICATION UMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300.6 FILLING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (703)836-9300
TELECAX: (703)838-4109
                                                                                                        TELEX: 899149

INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                  IMMEDIATE SOURCE:
CLONE: pTZgpt-
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CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
                                                             STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1097 RRRRRRRRRR 1087
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     STATE: V..
STATE: V..
COUNTRY: USA
COUNTRY: 22313-0299
TTD: 22313-0299
TTD: 273DABLE F
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                                           REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                           APPLICATION NUMBER: EP 91
FILING DATE: 26 AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.7
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                      CLASSIFICATION: 435
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Matches 26
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Patent No. 6159477
                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-06-23
NUMBER OF SEO ID NOS: 31
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 1
LENGTH: 6216
                                                                                                                                                                                                                                                                                                                         APPLICANT: AUDUONNET, Jean-Christophe
APPLICANT: BAUDU, Philippe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE,
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
CURRENT EILVENTION: PARKINFLUENZA 2 VIRUS
FILE REFERENCE: 454313-2200
CURRENT FILING NUMBER: US/09/213,053
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 9608242
EARLIER APPLICATION NUMBER: POT/TR97/01115
EARLIER APPLICATION NUMBER: POT/TR97/01115
                                                                                                                             Query Match
Best Local Similarity
Matches 111; Conserv
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LENGTH: 7218 base pairs
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CLONE: pTZgpt-
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                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Canine herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1453
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STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                   1994 agcottgootttaaaacootgaatoagcattotagogatgotgataagaagtaaatatago 2053
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                                                              2054 cacaatagagcggccattttccattcacatacagctcatcatgtgatcaatatcaagtat 2113
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26; Conserv
aactacaaaatcacttctatgtattggacttcaagctggaattttaacagccttaattat 3215
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linear
                                                                                                                               Conservative
                                                                                                                                                1.5%;
                                                                                                                                  Score 36.6; DB 3;
pred. No. 0.78;
0; Mismatches 124;
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; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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APPLICANT: Szostak, Jack W.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Roberts, Richard W
APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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; LCCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C
US-09-244-796-17
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US-09-103-840A-2
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SEQ ID NO 2
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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Best Local
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DUBBRCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 00/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                    LENGTH: 44
TYPE: DNA
              OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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OTHER INFORMATION: Translation template
                                                                            ORGANISM: Mycobacterium tuberculosis FEATURE:
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                                                                                                                                         4403765
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Pred. No. 0.19; 
93; Mismatches 113; Indels
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Query Match Best Local Similarity

1.4%;
48.7%;

Score 35.8; Pred. No. 39;

DB

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Length 4403765;

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PCT-US95-17083-9/c
Sequence 9, Application PC/TUS9517083
; GENERAL INFORMATION:
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APPLICANT: FLEISCHMAN, ROBERT D.

APPLICANT: WHITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: FRASER, Claire M.

APPLICANT: VENUER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
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FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/9/103,840A
NUMBER OF CTO 1998-06-34
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Best Local Similarity 48.7%;
Matches 97; Conservative
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               APPLICANT:
TITLE OF INVENTION: SECRING OF SEQUENCES: 16
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               633 gatagccactgcgggcggcgcatggctgatgatgtgcgccatgaaatgcggctggccga 692
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APPLICATION NUMBER:
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Pred. No. 39;
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PCT-US95-17083-7/c
; Sequence 7, Application PC/TUS9517083
; GENERAL INFORMATION:
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RESULT 10
PCT-US95-17083-5/c
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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STRANDEDNESS: single
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Local Similarity 50.9%;
nes 84; Conservative
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RENTLY HEREWITH
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pred. No. 0.57;
0; Mismatches 81;
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GENERAL INFORMATION:
APPLICANT:
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Best Local :
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INFORMATION FOR SEQ ID NO: 5:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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LENGTH: 975 base pairs
TYPE: nucleic acid
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CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
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988 AATTTGTTGTTTTTCACTCTAGACCAAGCTTTGGATTTCATTTCTGAAGTTTGAATTTTC
                                                                                                                                                                                                                                            LENGTH: 1104 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                  gtttttgtatttctaagtgctaacataactatcgctggccctaaagaagattgtactatt 2228
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                                                                 AGTATTTACAGCCAGCTATTAAGAATCTTTTCAAACACTAATTGCATATACTCAGAACTG
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                                                                                                                                     Conservative
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                                                                                                                                   Score 35.4; DB Pred. No. 0.66; 0; Mismatches
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US-08-444-231-18/c
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Best Local Similarity
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FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 1
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TITLE OF INVENTION: SECRETED HOWER, NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
APPLICATION CONCURRENTLY HEREWITH
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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LENGTH: 1167 base pairs
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APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF
TITLE OF INVENTION: THEREOF
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PRIOR APPLICATION DATA:
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                APPLICATION NUMBER: US/08/444,231 FILING DATE: 18-MAY-1995 CLASSIFICATION: 530
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CITY: Palo Alto
STATE: California
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                                                                                                                                                                                            ZIP: 94304-1018
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50.9%;
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                                                                                          Release #1.0,
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Pred. No. 0.
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APPLICATION NUMBER: US 08/152,443 FILING DATE: 15-NOV-1993 ATTORNEY/AGENT INFORMATION:

LEHNHARDT,

SUSAN K

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; LOCATION:
US-08-444-231-18
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
FRINGTH: 2471 base pairs
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Best Local Similarity 50.9
Matches 84; Conservative
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REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
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                             APPLICATION NUMBER: US/O.
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPPY
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS
TITLE OF INVENTION: THERBOF
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CORRESPONDENCE ADDRESS:
                                                                                                                     CURRENT APPLICATION DATA:
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                  REGISTRATION NUMBER:
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            LEHNHARDT, SUSAN K.
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(415) 494-0792
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NUMBER:
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 23647-20006.00
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US-08-219-237B-1/c
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Best Local Similarity
Matches 84; Conserv
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                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 1:
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                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
NAME: James W. Hellwege
28,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, MAOto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 22-APR-
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: James W.
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                SEQUENCE CHARACTERISTICS:
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LOCATION:
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LOCATION:
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TELEX: 706141
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CITY: Arlington
STATE: Virginia
                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 28-MAR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nilarity 50.9%;
Conservative
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2534 base pairs
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243
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Pred. No. 1.
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FEATURE:

NAME/KEY: POLYA_SITE

COCATION: 2518..2523

IDENTIFICATION METHOD:

IDENTIFICATION METHOD:

US-08-219-237B-1
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Search completed: August 21,
Job time: 18100 sec
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Best Local Similarity 50.9
Matches 84; Conservative
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NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to n
ORIGINAL SOURCE:
                                                                                                                                                   1220
                                                                                1160 TGAGTCACTAGTAATGTCCTTGAGGATGATAGTCTGAATTTTCTC 1116
                                                                                                   2229 gcagtatctcaccttgggtttcagaccgataattacagctttgtc 2273
                                                                                                                                                                     2169 gtttttgtatttctaagtgctaacataactatcgctggccctaaagaagattgtactatt 2228
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LIBRARY: PCEV4
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LOCATION: 195..1202
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Maximum DB seq
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

l (bases 1 to 442)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=&t2=CM1-LT0067-280
100-109-h11&t3=2000-01-28&t4=1)
Seq.primer: puc 18 forward AWB39280 442 bp mRNA linear CM1-LT0067-280100-109-hll LT0067 Homo sapiens cDNA, AWB39280 High quality sequence start: 37
High quality sequence stop: 442
Location/Qualifiers Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Contact: Simpson A.J.G. 20202663 sequence tags Shotgun sequencing of the human transcriptome with ORF expressed Simpson, A.J. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens AW839280.1 GI:7933254 Tel: +55-11-2704922 Fax: +55-11-2707001 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Natl. Acad. Sci. U.S.A. /organism="Homo sapiens" 97 (7), 3491-3496 (2000) mRNA sequence.

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                                                                                         FMAX: +33-14 Z. .....
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
This sequence was derived from the following URL
                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                        (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-151200-013-h06&t3=2000-12-15&t4=1)
Seq_primer: puc 18 forward
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Eutheria;
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/db_xref="taxon:9606"
/clone_lib="NN1200"
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/dev_stage="Adult"
/note="Organ: nervo
                                   /clone_lib="NN0219"
                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                 Location/Qualifiers
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nervous_normal;
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AGCATTTCCTTCTGGTCCAGCCTCTCCGTCTTGTCCAGCTTGTCCTGGTTGTCCGTCTGG 142
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                                                                                                                                                                                                                                                                                                                                                                                                Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                    Yata 1111, Mishima, Shizuoka 411, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biology Lab.
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans
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                                                                   h 1.8%;
Similarity 68.1%;
62; Conservative
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                                                                                                                                                                                                                                                                                                                                                         ykohara@lab.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                       /clone_lib="Yuji Kohara unpublished
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
/dev_stage="varied" 71 t
                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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Pred. No. 0.095;
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201 CGGGGCTGTC
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1 (bases 1 to 269)

Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-NNO219-
281000-004-a04&t3=2000-10-28&t4=1)
Seq_primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-NN0219-
281000-006-gl1&t3=2000-10-28&t4=1)
Seq primer: puc 18 forward
Lite Control of the contro
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bala, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dias Neto, E.,
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Mammalia; Eutheria;
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                                                                                                 ga59a02.y1 moss EST library PPŪ Physcomitrella patens cDNA clone
PEP_SOURCE_ID:PPU090903 5', mRNA sequence.
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                                                                                                                                                                         AW497369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence start: 59
quality sequence stop: 311.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                      272
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/clone_lib="NN0219"
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Query Match
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Libraries were constructed by Dr. Stavros Bashiardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco
High quality sequence stop: 372.
Location/Qualifiers
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Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
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Physcomitrella patens
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                              130
                                                                                                                                                    synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhoI. The result is CDNA with an EcoRI sticky end on one side and a XhoI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XLIBlue MRF' cells and amplified. The library was grown in XLIBlue MRF' cells and amplified. The library was grown in XLIBlue MRF' cells and amplified that releases the pBluescript sequence and circularises that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Quiagen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhOI; Construction of the cDNA library was carried out using Strategenes 'Unizap - cDNA synthesis kit'. cDNA was constructed using an oligo dT primer/linker that contains a XhOI site within it. Following ds cDNA synthesis, EcoRI adapters were ligated to the blunt ends synthesis, EcoRI adapters were ligated to the blunt ends
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/clone_lib="Moss EST library PPU"
/tissue_type="protonemata: 7 day old tissue
ammonium-grown"
/lab_host="PH10B"
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/db_xref="taxon:3218"
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Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood
      Score 44; DB 9 Pred. No. 0.19;
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                                                                                                                                 191 TTATCGTGCTTGTCCT 176
                                                                                                                                                                                                                 251 TCCTTCTTGTCGTGCTTGTCCTCCTTGTCATGCTTGTCCTTCTTATCGTGCTTGTCCTTC 192
                                                                                                                                                                         254 ttgtcccgcctgtcct 269
                                                                                                                                                                                                                                                                                                                            Local
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Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
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                                                                                                                                                                                                                                                                                                      Conservative
  normalized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
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73.7%;
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Pred. No.
  501 bp
length
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cDNA library,
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                        mRNA
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                                                                                                                                                                                                                                                                                                                                          Length 497;
                      linear
  chloronemata
                      EST 24-JAN-2002
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AUTHORS
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Best Local S
Matches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 56; Conser
                                                                                                                                                                                               BJ179016 546 bp mRNA lipsyl179016 normalized full length cDNA library, caulonemata and malformed buds Physcomitrella
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Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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Center For Genetic Resource Information
National Institute of Genetics
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Fujita, T., Shin-1, T
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Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
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Unpublished (2002)
                                                                                                                                BJ179016.1
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Fax: 81-559-81-6855
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                                                                                                                                                                           cDNA clone pphb24i04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp
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Carninci,P., Hayashizaki,Y.,
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105 c 15
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/tissue_type="mixture of chloronemata, caulonemata and
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                                                                                                                                GI:18346970
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0; Mismatches
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Shinozaki,K.,
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K., Kohara,Y. and Hasebe
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y, chloronemata,
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KEYWORDS
SOURCE
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BJ197576/C
LOCUS
DEFINITION
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AUTHORS
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                    COMMENT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttgtcccgcctgtcct 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56;
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                                                                                                                                              Physcomitrella patens subsp. patens.

Physcomitrella patens subsp. patens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 548)
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BJ197576.1 GI:18365499
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Unpublished (2002)
Contact: Tadasu Shin-i
               Comparison of the moss plants genome Unpublished (2002) Contact: Tadasu Shin-i
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                                                                                                                Fujita, T., Shin-i, T., Seki, M., Carninci, P., Hayashizaki, Y.,
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Fujita,T., Shin-i,T., Seki,M.,
Carninci,P., Hayashizaki,Y.,
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For Genetic Resource Information
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/db_xref="taxon:145481"
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/tissue_type="mixture of chloronemata, caulonema
malformed buds"
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Pred. No. 0.24
0; Mismatches
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                                                                                                                Kamiya,A., Uchiyama,I., Nishiyama,T. Shinozaki,K., Kohara,Y. and Hasebe
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A backbone of the vector is p
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from
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                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
                                                                                                                                                         Contact: Simpson A.J.G.
                                                                                                                                                                                                                    sequence tags
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73.7%;
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A backbone of the vector is phluescript II, that was in vivo excised from a modified IPS phage vector (Mo bi Tec, Germany). XhoI digested-5' end of cDNA is ligated to Sall site of the vector, and the BanHI digested-3' end including poly-A tail is ligated to BanHI conventional T7 and T3 primers. This normarized full-length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing lum NAA (naphthalene acetic acid) for 8 to 11 days under the continuous light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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/organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
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116 c 165 g 104 t

194 ttctgcctgtcgggcttgtcgggcttgtcggggcttgtcggggcttgtcgggcctgtccctc 253 249 TOCTTOTTGTCGTGCTTGTCCTTGTCATGCTTGTCCTTCTTATCGTGCTTGTCCTTC 190 Score 44; DB Pred. No. 0.24 0; Mismatches DB 10; 0.24; 20; Length 0, Gaps 0

217 bp mRI PM1-NN1200-190201-018-h03 NN1200 Homo B1033579 mRNA sapiens cDNA, linear mRNA sequence.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 217)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,F., Jongeneel,C.V., O'Hare,M.J., Soures,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson, A. J. Shotgun sequencing of the human $\operatorname{transcriptome}$ with ORF expressed (7), 3491-3496 (2000)

the FAPESP/LICR Human Cancer Genome

01509-010,

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AZ675008/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1200-190201-018-h03&t3-2001-02-19&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                      Email: bjloftus@tigr.org Clones are derived from
                                                                                                                                                                                                                                                                                                               Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 844)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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Entamoeba histolytica
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AZ675008.1 GI:11812154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue mRNA and cDNA amplification were performed under low stringency conditions." 39\ c 101\ g 39\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1200"
/dev_stage="Adult"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
                                                                                  /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
                                                                                                                                                Location/Qualifiers
                                                               /db_xref="taxon:5759"
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web : This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T3 end of clone BD0AA007C03 of library BD0AA from strain CBS Candida tropicalis, genomic survey sequence.
AL439691
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                                                                                                                                                                                                                                                                                                                                                                   Genoscope
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Saccharomycetales; mitosporic Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutleleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutleleostomi;

Mammalia; Eutlberia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 228)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Busai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

,M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
50; Conserv
                                                                                                                                                               Tel: +55-11-2704922

Tel: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/Scripts/gethtml2.pl?tl=PMI&t2=PMI-NN1200-271100-008-f12&t3=2000-11-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 163.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 97 (7), 20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF957901.1 GI:12375176
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Shotgun sequencing of the human transcriptome with ORF expressed
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/clone="bbhaA007C03"
/clone="
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/strain="CBS 94"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1200"
/dev_stage="Adult"
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8; Mismatches
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Inote="Organ: nervous_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NC. 196.716 - Ludwig Institute for Cancer Research) profiles into the puC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

2 others

BASE COUNT ORIGIN 27

Query Match Best Local S Matches 56 Similarity Conservative 1.7%; Score 42.8; D Pred. No. 0.32 0; Mismatches 0; DB (32) 10; Indels Length 0; Gaps

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рь 189 atagtttctgcctgtcgggcttgtcggggcttgtcggggcttgtcggggcttgtcgggcctgt 248 88 ATCATCCCTGGCTGTCGGGCTAGTCGGGGCTGTCGGGGCTAGT 147

QYВ 148 CGGGGCTGTCGGGCTAGT 165 249 ccctcttgtcccgcctgt 266 Qy

Search completed: August 20, 2002, 20:26:55 Job time: 5532 sec

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